

SEQUENCE LISTING

<110> O'Donnell, Michael E.
Yuzhakov, Alexander
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Bruck, Irina
Kuriyan, John

<120> ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
USE THEREOF

<130> 22221/1030

<140> 09/716,964
<141> 2000-11-21

<150> 60/143,202
<151> 1997-04-08

<150> 08/823,407
<151> 1997-04-08

<150> 09/057,416
<151> 1998-04-08

<160> 212

<170> PatentIn Ver. 2.1

<210> 1
<211> 2007
<212> DNA
<213> *Thermus thermophilus*

<400> 1
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 gatgaccgccc accaagaagg ccatggaggc ggcggccacc ctgatcctcc acgagttcct 1920
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<210> 2
 <211> 529
 <212> PRT
 <213> *Thermus thermophilus*

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 1 5 10 15
 Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
 20 25 30
 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
 35 40 45
 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 50 55 60
 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65 70 75 80
 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
 85 90 95

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
 100 105 110
 Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
 115 120 125
 Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
 130 135 140
 His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
 145 150 155 160
 Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
 165 170 175
 Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
 180 185 190
 Glu Ala Glu Glu Ala Leu Leu Leu Ala Arg Leu Ala Asp Gly
 195 200 205
 Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
 210 215 220
 Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
 225 230 235 240
 Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
 245 250 255
 Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
 260 265 270
 Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
 275 280 285
 Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
 290 295 300
 Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
 305 310 315 320
 Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
 325 330 335
 Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
 340 345 350

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
355 360 365

Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
370 375 380

Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
385 390 395 400

Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
405 410 415

Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
420 425 430

Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
435 440 445

Gly Glu Lys Lys Ser Leu Ser Pro Arg Pro Arg Pro Ala Pro Pro Pro
450 455 460

Glu Ala Pro Ala Pro Pro Gly Pro Pro Glu Glu Val Glu Ala Glu
465 470 475 480

Glu Ala Ala Glu Glu Ala Pro Glu Glu Ala Leu Arg Arg Val Val Arg
485 490 495

Leu Leu Gly Gly Arg Val Leu Trp Val Arg Arg Pro Arg Thr Arg Glu
500 505 510

Ala Pro Glu Glu Glu Pro Leu Ser Gln Asp Glu Ile Gly Thr Gly
515 520 525

Ile

<210> 3

<211> 1590

<212> DNA

<213> *Thermus thermophilus*

<400> 3

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ttctccgggc ccagggcgt gggcaagacc accacggcga ggctcctcgc catggcggtg 180
gggtgccagg gggaaagaccc cccttgcggg gtctgcccc actgccaggc ggtgcagagg 240

ggcgccacc cggacgtggt ggacattgac gccgccagca acaactccgt ggaggacgtg 300
 cggagctga gggaaaggat ccacctcgcc cccctctctg cccccagggaa ggtcttcatc 360
 ctggacgagg cccacatgct ctccaaaagc gccttcaacg ccctcctcaa gaccctggag 420
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 accatcctct cccgcaccca gcacttccgc ttccgcccgc tcacggagga ggagatcgcc 540
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 gggaccgggg tggccgagat cgccgcctcc ctgcgcgggg ggaaaacggc ggaggccctg 780
 ggccctcgccc ggccgcctcta cggggaaaggg tacgccccga ggagcctggt ctcggccctt 840
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 gaaagccccc cgaccccgga acccccaagg cccgaggagg cgcccgaccc gcgggagcgg 1140
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 caagacgaga tagggggtaa tggtatataa 1590

<210> 4

<211> 464

<212> PRT

<213> *Thermus thermophilus*

<400> 4

Met Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
 1 5 10 15

Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
 20 25 30

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
 35 40 45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 50 55 60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65 70 75 80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
 85 90 95

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
 100 105 110
 Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
 115 120 125
 Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
 130 135 140
 His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
 145 150 155 160
 Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
 165 170 175
 Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
 180 185 190
 Glu Ala Glu Glu Ala Leu Leu Leu Ala Arg Leu Ala Asp Gly
 195 200 205
 Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
 210 215 220
 Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
 225 230 235 240
 Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
 245 250 255
 Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
 260 265 270
 Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
 275 280 285
 Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
 290 295 300
 Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
 305 310 315 320
 Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
 325 330 335
 Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
 340 345 350

Ser	Pro	Glu	Val	Gly	Pro	Lys	Pro	Glu	Ser	Pro	Pro	Thr	Pro	Glu	Pro		
355																	
														360	365		
Pro	Arg	Pro	Glu	Glu	Ala	Pro	Asp	Leu	Arg	Glu	Arg	Trp	Arg	Ala	Phe		
370															375	380	
Leu	Glu	Ala	Leu	Arg	Pro	Thr	Leu	Arg	Ala	Phe	Val	Arg	Glu	Ala	Arg		
385															390	395	400
Pro	Glu	Val	Arg	Glu	Gly	Gln	Leu	Cys	Leu	Ala	Phe	Pro	Glu	Asp	Lys		
															405	410	415
Ala	Phe	His	Tyr	Arg	Lys	Ala	Ser	Glu	Gln	Lys	Val	Arg	Leu	Leu	Pro		
															420	425	430
Leu	Ala	Gln	Ala	His	Phe	Gly	Val	Glu	Glu	Val	Val	Leu	Val	Leu	Glu		
															435	440	445
Gly	Glu	Lys	Lys	Lys	Pro	Glu	Pro	Lys	Ala	Pro	Pro	Gly	Pro	Thr	Ser		
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<210> 5
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 <212> PRT
 <213> *Thermus thermophilus*

<400> 5																		
Met	Ser	Ala	Leu	Tyr	Arg	Arg	Phe	Arg	Pro	Leu	Thr	Phe	Gln	Glu	Val			
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															20	25	30	
Gly	Arg	Leu	Ala	Gln	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly	Val	Gly			
															35	40	45	
Lys	Thr	Thr	Thr	Ala	Arg	Leu	Leu	Ala	Met	Ala	Val	Gly	Cys	Gln	Gly			
															50	55	60	
Glu	Asp	Pro	Pro	Cys	Gly	Val	Cys	Pro	His	Cys	Gln	Ala	Val	Gln	Arg			
															65	70	75	80
Gly	Ala	His	Pro	Asp	Val	Val	Asp	Ile	Asp	Ala	Ala	Ser	Asn	Asn	Ser			

85

90

95

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
100 105 110

Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
115 120 125

Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
130 135 140

His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
145 150 155 160

Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
165 170 175

Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
180 185 190

Glu Ala Glu Glu Ala Leu Leu Leu Ala Arg Leu Ala Asp Gly
195 200 205

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
210 215 220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
225 230 235 240

Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
245 250 255

Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
260 265 270

Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
275 280 285

Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
290 295 300

Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
305 310 315 320

Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
325 330 335

Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro

340

345

350

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
355 360 365

Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
370 375 380

Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
385 390 395 400

Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
405 410 415

Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
420 425 430

Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
435 440 445

Gly Glu Lys Lys Lys Ala
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<210> 6

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 6

32

cgcaagcttc acgcstacct sttctccggs ac

<210> 7

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 7

His Ala Tyr Leu Phe Ser Gly Thr

1

5

<210> 8
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 8
cgcgaaatcg tgctcsggsg gctcctcsag sgtc

34

<210> 9
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 9
Lys Thr Leu Glu Glu Pro Pro Glu His
1 5

<210> 10
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 10
gcgcggatcc ggagggagaa aaaaaaagcc tcagccca

38

<210> 11
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 11
gcgcggatcc ggagggagag aagaaaagcc tcagccca

38

<210> 12
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 12
gaattaaatt cgcgcttcgg gaggtggg 28

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 13
gcgcgaattc gcgcgttcggg aggtggg 27

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
gcgcgaattc gggcgcttca ggaggtggg 29

<210> 15
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 15
gtggtgacata tggtgagcgc cctctaccgc c 31

<210> 16
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 16
gtggtgtcg acccaggagg gccacacctcca g

31

<210> 17
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

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<221> PEPTIDE
<222> (2)
<223> X is any aa at position 2

<220>
<221> PEPTIDE
<222> (3)
<223> X is any aa at position 3

<220>
<221> PEPTIDE
<222> (5)
<223> X is any aa at position 5

<400> 17
Gly Xaa Xaa Gly Xaa Gly Lys Thr
1 5

<210> 18
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 18

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1 5 10

<210> 19

<211> 180

<212> PRT

<213> Escherichia coli

<400> 19

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala
1 5 10 15

Asp Val Val Gly Gln Glu His Val Leu Thr Ala Leu Ala Asn Gly Leu
20 25 30

Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
50 55 60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
65 70 75 80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
100 105 110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Ala Leu Asp Val
180

<210> 20
<211> 180
<212> PRT
<213> *Bacillus subtilis*

<400> 20
Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu
1 5 10 15
Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu
20 25 30
Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
35 40 45
Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
50 55 60
Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys
65 70 75 80
Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala
85 90 95
Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys
100 105 110
Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val
115 120 125
His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140
Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His
145 150 155 160
Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys
165 170 175
Arg Ile Thr Ser
180

<210> 21
<211> 294
<212> PRT

<213> Escherichia coli

<400> 21
Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala
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Asp Val Val Gly Gln Glu His Val Leu Thr Ala Leu Ala Asn Gly Leu
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Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45
Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
50 55 60
Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
65 70 75 80
Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95
Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
100 105 110
Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125
His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140
Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160
Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175
Ala Leu Asp Val Glu Gln Ile Arg His Gln Leu Glu His Ile Leu Asn
180 185 190
Glu Glu His Ile Ala His Glu Pro Arg Ala Leu Gln Leu Leu Ala Arg
195 200 205
Ala Ala Glu Gly Ser Leu Arg Asp Ala Leu Ser Leu Thr Asp Gln Ala
210 215 220
Ile Ala Ser Gly Asp Gly Gln Val Ser Thr Gln Ala Val Ser Ala Met
225 230 235 240

Leu Gly Thr Leu Asp Asp Asp Gln Ala Leu Ser Leu Val Glu Ala Met
245 250 255

Val Glu Ala Asn Gly Glu Arg Val Met Ala Leu Ile Asn Glu Ala Ala
260 265 270

Ala Arg Gly Ile Glu Trp Glu Ala Leu Leu Val Glu Met Leu Gly Leu
275 280 285

Leu His Arg Ile Ala Met
290

<210> 22

<211> 294

<212> PRT

<213> Haemophilus influenzae

<400> 22
Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Lys Thr Phe Ala
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Asp Val Val Gly Gln Glu His Ile Ile Thr Ala Leu Ala Asn Gly Leu
20 25 30

Lys Asp Asn Arg Leu His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Phe Ala Lys Gly Leu Asn Cys
50 55 60

Val His Gly Val Thr Ala Thr Pro Cys Gly Glu Cys Glu Asn Cys Lys
65 70 75 80

Ala Ile Glu Gln Gly Asn Phe Ile Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Glu Leu Leu Asp Asn Val Gln
100 105 110

Tyr Lys Pro Val Val Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu Tyr Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Ala Leu Asp Glu Thr Gln Ile Ser Gln His Leu Ala His Ile Leu Thr
180 185 190

Gln Glu Asn Ile Pro Phe Glu Asp Pro Ala Leu Val Lys Leu Ala Lys
195 200 205

Ala Ala Gln Gly Ser Ile Arg Asp Ser Leu Ser Leu Thr Asp Gln Ala
210 215 220

Ile Ala Met Gly Asp Arg Gln Val Thr Asn Asn Val Val Ser Asn Met
225 230 235 240

Leu Gly Leu Leu Asp Asp Asn Tyr Ser Val Asp Ile Leu Tyr Ala Leu
245 250 255

His Gln Gly Asn Gly Glu Leu Leu Met Arg Thr Leu Gln Arg Val Ala
260 265 270

Asp Ala Ala Gly Asp Trp Asp Lys Leu Leu Gly Glu Cys Ala Glu Lys
275 280 285

Leu His Gln Ile Ala Leu
290

<210> 23

<211> 294

<212> PRT

<213> *Bacillus subtilis*

<400> 23
Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu
1 5 10 15

Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu
20 25 30

Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
35 40 45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
50 55 60

Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys

65	70	75	80
Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala			
85	90		95
Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys			
100	105		110
Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val			
115	120		125
His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu			
130	135		140
Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His			
145	150	155	160
Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys			
165	170		175
Arg Ile Thr Ser Gln Ala Ile Val Gly Arg Met Asn Lys Ile Val Asp			
180	185		190
Ala Glu Gln Leu Gln Val Glu Glu Gly Ser Leu Glu Ile Ile Ala Ser			
195	200		205
Ala Ala His Gly Gly Met Arg Asp Ala Leu Ser Leu Leu Asp Gln Ala			
210	215		220
Ile Ser Phe Ser Gly Asp Ile Leu Lys Val Glu Asp Ala Leu Leu Ile			
225	230	235	240
Thr Gly Ala Val Ser Gln Leu Tyr Ile Gly Lys Leu Ala Lys Ser Leu			
245	250		255
His Asp Lys Asn Val Ser Asp Ala Leu Glu Thr Leu Asn Glu Leu Leu			
260	265		270
Gln Gln Gly Lys Asp Pro Ala Lys Leu Ile Glu Asp Met Ile Phe Tyr			
275	280	285	
Phe Arg Asp Met Leu Leu			
290			

<210> 24
 <211> 300
 <212> PRT

<213> Caulobacter crescentus

<400> 24
Asp Ala Tyr Thr Val Leu Ala Arg Lys Tyr Arg Pro Arg Thr Phe Glu
1 5 10 15
Asp Leu Ile Gly Gln Glu Ala Met Val Arg Thr Leu Ala Asn Ala Phe
20 25 30
Ser Thr Gly Arg Ile Ala His Ala Phe Met Leu Thr Gly Val Arg Gly
35 40 45
Val Gly Lys Thr Thr Ala Arg Leu Leu Ala Arg Ala Leu Asn Tyr
50 55 60
Glu Thr Asp Thr Val Lys Gly Pro Ser Val Asp Leu Thr Thr Glu Gly
65 70 75 80
Tyr His Cys Arg Ser Ile Ile Glu Gly Arg His Met Asp Val Leu Glu
85 90 95
Leu Asp Ala Ala Ser Arg Thr Lys Val Asp Glu Met Arg Glu Leu Leu
100 105 110
Asp Gly Val Arg Tyr Ala Pro Val Glu Ala Arg Tyr Lys Val Tyr Ile
115 120 125
Ile Asp Glu Val His Met Leu Ser Thr Ala Ala Phe Asn Ala Leu Leu
130 135 140
Lys Thr Leu Glu Glu Pro Pro His Ala Lys Phe Ile Phe Ala Thr
145 150 155 160
Thr Glu Ile Arg Lys Val Pro Val Thr Ile Leu Ser Arg Cys Gln Arg
165 170 175
Phe Asp Leu Arg Arg Val Glu Pro Asp Val Leu Val Lys His Phe Asp
180 185 190
Arg Ile Ser Ala Lys Glu Gly Ala Arg Ile Glu Met Asp Ala Leu Ala
195 200 205
Leu Ile Ala Arg Ala Ala Glu Gly Ser Val Arg Asp Gly Leu Ser Leu
210 215 220
Leu Asp Gln Ala Ile Val Gln Thr Glu Arg Gly Gln Thr Val Thr Ser
225 230 235 240

Thr Val Val Arg Asp Met Leu Gly Leu Ala Asp Arg Ser Gln Thr Ile
245 250 255

Ala Leu Tyr Glu His Val Met Ala Gly Lys Thr Lys Asp Ala Leu Glu
260 265 270

Gly Phe Arg Ala Leu Trp Gly Phe Gly Ala Asp Pro Ala Val Val Met
275 280 285

Leu Asp Val Leu Asp His Cys His Ala Ser Ala Val
290 295 300

<210> 25

<211> 260

<212> PRT

<213> Mycoplasma genitalium

<400> 25

Met His Gln Val Phe Tyr Gln Lys Tyr Arg Pro Ile Asn Phe Lys Gln
1 5 10 15

Thr Leu Gly Gln Glu Ser Ile Arg Lys Ile Leu Val Asn Ala Ile Asn
20 25 30

Arg Asp Lys Leu Pro Asn Gly Tyr Ile Phe Ser Gly Glu Arg Gly Thr
35 40 45

Gly Lys Thr Thr Phe Ala Lys Ile Ile Ala Lys Ala Ile Asn Cys Leu
50 55 60

Asn Trp Asp Gln Ile Asp Val Cys Asn Ser Cys Asp Val Cys Lys Ser
65 70 75 80

Ile Asn Thr Asn Ser Ala Ile Asp Ile Val Glu Ile Asp Ala Ala Ser
85 90 95

Lys Asn Gly Ile Asn Asp Ile Arg Glu Leu Val Glu Asn Val Phe Asn
100 105 110

His Pro Phe Thr Phe Lys Lys Val Tyr Ile Leu Asp Glu Ala His
115 120 125

Met Leu Thr Thr Gln Ser Trp Gly Gly Leu Leu Lys Thr Leu Glu Glu
130 135 140

Ser Pro Pro Tyr Val Leu Phe Ile Phe Thr Thr Glu Phe Asn Lys
145 150 155 160

Ile Pro Leu Thr Ile Leu Ser Arg Cys Gln Ser Phe Phe Phe Lys Lys
165 170 175

Ile Thr Ser Asp Leu Ile Leu Glu Arg Leu Asn Asp Ile Ala Lys Lys
180 185 190

Glu Lys Ile Lys Ile Glu Lys Asp Ala Leu Ile Lys Ile Ala Asp Leu
195 200 205

Ser Gln Gly Ser Leu Arg Asp Gly Leu Ser Leu Leu Asp Gln Leu Ala
210 215 220

Ile Ser Leu Ile Val Lys Lys Leu Val Leu Leu Met Leu Lys Lys His
225 230 235 240

Leu Ile Ser Leu Ile Glu Met Gln Asn Leu Leu Leu Lys Gln Phe
245 250 255

Tyr Gln Glu Ile
260

<210> 26

<211> 289

<212> PRT

<213> Thermus thermophilus

<400> 26

Val Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
1 5 10 15

Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
20 25 30

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
35 40 45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
50 55 60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
65 70 75 80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
85 90 95

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu

100	105	110
Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser		
115	120	125
Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro		
130	135	140
His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro		
145	150	160
Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu		
165	170	175
Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg		
180	185	190
Glu Ala Glu Glu Ala Leu Leu Leu Ala Arg Leu Ala Asp Gly		
195	200	205
Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu		
210	215	220
Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro		
225	230	240
Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr		
245	250	255
Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala		
260	265	270
Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu		
275	280	285
Tyr		

<210> 27
 <211> 94
 <212> DNA
 <213> *Thermus thermophilus*

<400> 27
 gccggaggga gaaaaaaaaa gccgagccca aggccccgcc cggccccacc ccgaagcgcc 60
 cgcaccccccggccccccgaa ggaggaggag aggcc 94

<210> 28
<211> 11
<212> PRT
<213> *Thermus thermophilus*

<400> 28
Val Leu Glu Gly Glu Lys Lys Ser Leu Ser Pro
1 5 10

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> (6)
<223> N at position 6 is either G or C

<220>
<221> unsure
<222> (12)
<223> N at position 12 is either G or C

<220>
<221> unsure
<222> (21)
<223> N at position 21 is either G or C

<400> 29
cacgcntacc tnttctccgg nac 23

<210> 30
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure

<222> (7)
<223> N at position 7 is either G or C

<220>
<221> unsure
<222> (10)
<223> N at position 10 is either G or C

<220>-
<221> unsure
<222> (19)
<223> N at position 19 is either G or C

<220>
<221> unsure
<222> (22)
<223> N at position 22 is either G or C

<400> 30
gtgctcnggn ggctcctcnt cngtc

25

<210> 31
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 31
gtgggatccg tggttctgga tctcgatgaa gaa

33

<210> 32
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 32
gtgggatcca cggsctstcs gagcagaag

29

<210> 33
<211> 34

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 33
gcgggatcct caacgaggac ctctccatct tcaa 34

<210> 34
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 34
gcgggatcct tgcgtcsag sgtsagsgcg tcgta 35

<210> 35
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 35
ggaaaggacc agcgctact cccccctgctc ctaggtgtg 39

<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 36
gtgtggatcc ttcttcttsc ccatsgc 27

<210> 37
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 37
caccgattcc agtgggtgcct aggtgtg 27

<210> 38
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 38
caacacacctgg tggccagga gcctgtgctt 30

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 39
ccagaatcgt ctgctggtcg tag 23

<210> 40
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 40
agcacccctgg aggagcttc 19

<210> 41
<211> 19

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 41
catgtcgtac tgggtgtac

19

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> (7)
<223> N at position 7 is A, C, G, or T

<220>
<221> unsure
<222> (8)
<223> N at position 8 is A, C, G, or T

<220>
<221> unsure
<222> (13)
<223> N at position 13 is A, C, G, or T

<220>
<221> unsure
<222> (14)
<223> N at position 14 is A, C, G, or T

<400> 42
gtsgtsnnsg acnnsgagac sacsggg

27

<210> 43
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> (8)
<223> N at position 8 is A, C, G, or T

<220>
<221> unsure
<222> (9)
<223> N at position 9 is A, C, G, or T

<220>
<221> unsure
<222> (17)
<223> N at position 17 is A, C, G, or T

<220>
<221> unsure
<222> (18)
<223> N at position 18 is A, C, G, or T

<400> 43
gaasccsnng tcgaasnngg cgttgtg

27

<210> 44
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 44
cggggatcca cctcaatcac ctcgtgg

27

<210> 45
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 45
cggggatccg ccacccgtcg gctccgggtg

30

<210> 46
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 46
gcgctctaga cgagttccca aagcgtgcgg t 31

<210> 47
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 47
cgcgtctaga tcacctgtat ccaga 25

<210> 48
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 48
gccccgcata tggtggtggt cctggacctg gag 33

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 49
cgcgtctaga tcacctgtat ccaga 25

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 50
gtstcgtsa agacscactt 20

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 51
sagsagsgcg ttgaasgtgt g 21

<210> 52
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 52
ctcgttggtg aaagttccg tg 22

<210> 53
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 53
ctcgttggtg aaagttccg tg 22

<210> 54
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 54
tctggcaaca cgttctggag cacatcc

27

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 55
tgctggcggtt catcttcagg atg

23

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 56
catcctgaag atgaacgcca gca

23

<210> 57
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 57
aggttatcca caggggtcat gtgca

25

<210> 58
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 58
gtgtgtcata tgaacataac ggttcccaa 29

<210> 59
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 59
gcgcgaattc tcccttgtgg aaggcttag 29

<210> 60
<211> 13
<212> PRT
<213> Thermus thermophilus

<400> 60
Arg Val Glu Leu Asp Tyr Asp Ala Leu Thr Leu Asp Asp
1 5 10

<210> 61
<211> 14
<212> PRT
<213> Thermus thermophilus

<400> 61
Phe Phe Ile Glu Ile Gln Asn His Gly Leu Ser Glu Gln Lys
1 5 10

<210> 62
<211> 8

<212> PRT

<213> *Thermus thermophilus*

<400> 62

Phe Phe Ile Glu Ile Gln Asn His
1 5

<210> 63

<211> 8

<212> PRT

<213> *Thermus thermophilus*

<400> 63

Tyr Asp Ala Leu Thr Leu Asp Asp
1 5

<210> 64

<211> 6

<212> PRT

<213> *Thermus thermophilus*

<400> 64

Ala Met Gly Lys Lys Lys
1 5

<210> 65

<211> 9

<212> PRT

<213> *Thermus thermophilus*

<400> 65

Phe Asn Lys Ser His Ser Ala Ala Tyr
1 5

<210> 66

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<220>

<221> PEPTIDE

<222> (3)
<223> Xaa at position 3 is undefined

<220>
<221> PEPTIDE
<222> (5)
<223> Xaa at position 5 is undefined

<400> 66
Val Val Xaa Asp Xaa Glu Thr Thr Gly
1 5

<210> 67
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (4)
<223> Xaa at position 4 is undefined

<220>
<221> PEPTIDE
<222> (7)
<223> Xaa at position 7 is undefined

<400> 67
His Asn Ala Xaa Phe Asp Xaa Gly Phe
1 5

<210> 68
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (3)
<223> Xaa at position 3 is undefined

<220>
<221> PEPTIDE
<222> (5)
<223> Xaa at position 5 is undefined

<400> 68
Val Val Xaa Asp Xaa Glu Thr Thr Gly
1 5

<210> 69
<211> 7
<212> PRT
<213> Thermus thermophilus

<400> 69
Val Leu Val Lys Thr His Leu
1 5

<210> 70
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 70
His Arg Ala Leu Tyr Asp
1 5

<210> 71
<211> 7
<212> PRT
<213> Thermus thermophilus

<400> 71
His Thr Phe Asn Ala Leu Leu
1 5

<210> 72
<211> 34
<212> PRT
<213> Escherichia coli

<400> 72

Asp Arg Tyr Phe Leu Glu Leu Ile Arg Thr Gly Arg Pro Asp Glu Glu
1 5 10 15

Ser Tyr Leu His Ala Ala Val Glu Leu Ala Glu Ala Arg Gly Leu Pro
20 25 30

Val Val

<210> 73

<211> 34

<212> PRT

<213> Vibrio cholerae

<400> 73

Asp His Phe Tyr Leu Glu Leu Ile Arg Thr Gly Arg Ala Asp Glu Glu
1 5 10 15

Ser Tyr Leu His Phe Ala Leu Asp Val Ala Glu Gln Tyr Asp Leu Pro
20 25 30

Val Val

<210> 74

<211> 34

<212> PRT

<213> Haemophilus influenzae

<400> 74

Asp His Phe Tyr Leu Ala Leu Ser Arg Thr Gly Arg Pro Asn Glu Glu
1 5 10 15

Arg Tyr Ile Gln Ala Ala Leu Lys Leu Ala Glu Arg Cys Asp Leu Pro
20 25 30

Leu Val

<210> 75

<211> 34

<212> PRT

<213> Rickettsia prowazekii

<400> 75
Asp Arg Phe Tyr Phe Glu Ile Met Arg His Asp Leu Pro Glu Glu Gln
5 10 15
1
Phe Ile Glu Asn Ser Tyr Ile Gln Ile Ala Ser Glu Leu Ser Ile Pro
20 25 30

Ile Val

<210> 76
<211> 34
<212> PRT
<213> *Helicobacter pylori*

<400> 76
Asp Asp Phe Tyr Leu Glu Ile Met Arg His Gly Ile Leu Asp Gln Arg
1 5 10 15
Phe Ile Asp Glu Gln Val Ile Lys Met Ser Leu Glu Thr Gly Leu Lys
20 25 30

Ile Ile

<210> 77
<211> 34
<212> PRT
<213> *Synechocystis* sp.

<400> 77
Asp Asp Tyr Tyr Leu Glu Ile Gln Asp His Gly Ser Val Glu Asp Arg
1 5 10 15
Leu Val Asn Ile Asn Leu Val Lys Ile Ala Gln Glu Leu Asp Ile Lys
20 25 30

Ile Val

<210> 78
<211> 34
<212> PRT
<213> *Mycobacterium tuberculosis*

<400> 78
Asp Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Thr Ile Glu Arg
1 5 10 15

Arg Val Arg Asp Gly Leu Leu Glu Ile Gly Arg Ala Leu Asn Ile Pro
20 25 30

Pro Leu

<210> 79

<211> 46

<212> PRT

<213> Escherichia coli

<400> 79
Asn Lys Arg Arg Ala Lys Asn Gly Glu Pro Pro Leu Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Lys Lys Ser Phe Asp Met Leu Gln Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
35 40 45

<210> 80

<211> 46

<212> PRT

<213> Vibrio cholerae

<400> 80
Asn Pro Arg Leu Lys Lys Ala Gly Lys Pro Pro Val Arg Ile Glu Ala
1 5 10 15

Ile Pro Leu Asp Asp Ala Arg Ser Phe Arg Asn Leu Gln Asp Ala Lys
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu
35 40 45

<210> 81

<211> 46

<212> PRT

<213> Haemophilus influenzae

<400> 81

Asn Val Arg Met Val Arg Glu Gly Lys Pro Arg Val Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Pro Glu Ser Phe Glu Leu Leu Lys Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
35 40 45

<210> 82

<211> 46

<212> PRT

<213> Rickettsia prowazekii

<400> 82

Cys Lys Lys Leu Leu Lys Glu Gln Gly Ile Lys Ile Asp Phe Asp Asp
1 5 10 15

Met Thr Phe Asp Asp Lys Lys Thr Tyr Gln Met Leu Cys Lys Gly Lys
20 25 30

Gly Val Gly Val Phe Gln Phe Glu Ser Ile Gly Met Lys Asp
35 40 45

<210> 83

<211> 45

<212> PRT

<213> Helicobacter pylori

<400> 83

Leu Lys Ile Ile Lys Thr Gln His Lys Ile Ser Val Asp Phe Leu Ser
1 5 10 15

Leu Asp Met Asp Asp Pro Lys Val Tyr Lys Thr Ile Gln Ser Gly Asp
20 25 30

Thr Val Gly Ile Phe Gln Ile Glu Ser Gly Met Phe Gln
35 40 45

<210> 84

<211> 46

<212> PRT

<213> Synechocystis sp.

<400> 84

Gln Glu Arg Lys Ala Leu Gln Ile Arg Ala Arg Thr Gly Ser Lys Lys
1 5 10 15

Leu Pro Asp Asp Val Lys Lys Thr His Lys Leu Leu Glu Ala Gly Asp
20 25 30

Leu Glu Gly Ile Phe Gln Leu Glu Ser Gln Gly Met Lys Gln
35 40 45

<210> 85

<211> 46

<212> PRT

<213> *Mycobacterium tuberculosis*

<400> 85

Ile Asp Asn Val Arg Ala Asn Arg Gly Ile Asp Leu Asp Leu Glu Ser
1 5 10 15

Val Pro Leu Asp Asp Lys Ala Thr Tyr Glu Leu Leu Gly Arg Gly Asp
20 25 30

Thr Leu Gly Val Phe Gln Leu Asp Gly Gly Pro Met Arg Asp
35 40 45

<210> 86

<211> 3729

<212> DNA

<213> *Thermus thermophilus*

<400> 86

atggggccgggg agctccgctt cgccccaccc caccaggaca cccagttctc cctcctggac 60
ggggcggcga agctttccga cctcctcaag tgggtcaagg agacgacccc cgaggacccc 120
gccttggcca tgaccgacca cggcaaccc tcggggccg tggagttcta caagaaggcc 180
accgaaatgg gcatcaagcc catcctggc tacgaggcct acgtggcgc ggaaagccgc 240
tttgaccgca agcggggaaa gggcctagac gggggctact ttcacctcac cctcctcgcc 300
aaggacttca cggggtacca gaacctggtg cgccctggcga gccgggctta cctggagggg 360
ttttacggaa agccccggat tgaccgggag atcctgcgcg agcacccgcg gggcctcata 420
gccctctcgg ggtgcctcgg ggcggagatc ccccatgtca tcctccagga ccgtctggac 480
ctggccgagg cccggctcaa cgagtaccc tccatctca aggaccgctt cttcatcgag 540
atccagaacc acggccccc cgagcagaaa aaggtaacg aggtcctcaa ggagttcgcc 600
cgaaagtacg gcctggggat ggtggccacc aacgacggcc attacgtgag gaaggaggac 660
gccccgcgccc acgaggtcct cctcgccatc cagttcaaga gcaccctgga cgaccgggg 720
cgctggcgct tcccctgcga cgagtctac gtgaagaccc cccgaggat gcggggccatg 780
ttcccccggagg aggagtgggg ggacgagccc tttgacaaca ccgtggagat cgcccgcatg 840

tgcaacgtgg agctgcccatt cggggacaag atggtctacc gaatcccccg cttccccctc 900
cccgaggggc ggaccgaggc ccagtacctc atggagctca cttcaaggg gtcctccgc 960
cgctaccgg accggatcac cgaggccttc taccggagg tcttccgc tttggggaaag 1020
cttcccccc acggggacgg ggaggcctt gccgaggcct tggccaggt ggagcggag 1080
gcttggaga ggctcatgaa gacccccc ctttgccg ggtcaagga gtggacggcg 1140
gaggccatt tccaccggc ctttacgag ctttccgtga tagagcgtat ggggttccc 1200
ggctacttcc tcatacgcca ggactacatc aactggccc ggagaaacgg cgtctccgt 1260
ggggccggca gggggagcgc cgccgggagc ctggggcct acggcgtgg gatcaccaac 1320
attgacccccc tccgctcgg cttccctttt gagcgttcc tgaacccgaa gagggtctcc 1380
atgcccaca ttgacacgga ctctccgac cggagcggg accgggtat ccagtagtg 1440
cgggagcgt acggcgagga caaggtggcc cagatcgca ccctggaaag cctccctcc 1500
aaggccgccc tcaaggacgt gggccgggtc tacggcatcc cccacaagaa ggcggaggaa 1560
ttggccaagc tcataccggt gcagttcggg aagcccaagc ccctgcagga ggccatccag 1620
gtggtccgg agcttagggc ggagatggag aaggacccca aggtgcggg ggtctcgt 1680
gtggccatgc gcctggaggg cctgaaccgc cacgcctccg tccacgccc cgggggtgg 1740
atcgccgccc agccctcac ggacctcgtc cccctcatgc gcgaccagga agggcggccc 1800
gtcaccaggc acgacatggg ggcgggtggag gccttggggc ttttgaagat ggacttttg 1860
ggcctccgca ccctcacctt cctggacgag gtcaagcgtca tcgtcaaggc gtcccagggg 1920
gtggagctgg actacgatgc cttcccttg gacgacccca agacccctgc cttccctctcc 1980
cggggggaga ccaagggggt cttccagctg gagtcggggg ggtacccgc cacgctccgc 2040
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cccatggagc acatccccac ctacatccgc cgccaccacg ggctggagcc cgtgagctac 2160
agcgagttc cccacgcccga gaagtaccta aagcccatcc tggacgagac ctacggcatc 2220
cccgcttacc agaggcagat catgcagatc gcctcgccg tggcggggta ctccctggc 2280
gaggcggacc tcctcgccg gtccatggc aagaagaagg tggaggagat gaagtcccac 2340
cgggagcgt tcgtccaggg ggccaaggaa agggcggtgc ccgaggagga ggccaaccgc 2400
ctcttgcaca tgctggaggc cttcgccaaac tacggcttca acaaattccaa cgctgccc 2460
tacagcctcc tctcctacca gaccgcctac gtgaaggccc actaccctgt ggagttcatg 2520
gccgcctcc tctccgtgg gcggcacgac tccgacaagg tggccgagta catccgcac 2580
gcccgggcca tgggcataga ggtcttccc ccggacgtca accgctccgg gtttgacttc 2640
ctggtccagg gcccgcagat cttttcggc ctctccgcgg tgaagaacgt gggcgaggcg 2700
cgccggagg ccattctccg ggagcggggag cggggcgcc cctaccggag cctcggcgac 2760
ttcctcaagc ggctggacga gaaggtgctc aacaagcga ccctggagtc cctcatcaag 2820
cgccggccc tggacggctt cggggaaagg gcgcggctcc tcgcctccct ggaagggctc 2880
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tacgagaagg agggccctgg gatctacgtc tccggccacc ccatttgccg gtacccggg 3060
ctccgggaga cggccacctg caccctggag gagttcccc acctggccc ggacctgccc 3120
ccccggctta gggctctt tggccggatg gtggaggagg tggtcgcaaa gcccacaaag 3180
agccggggta tgatggccc cttcgcttcc tccgacgaga cggggggcgt tgaggcggtg 3240
gcattcgcc gggcctacga ccaggcttcc ccggaggctca aggaggacac ccccggtctc 3300
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acctacgagg agctggagca gttccccgg gcccgcagg tggaggtggaa ggctccctc 3420
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cccctgtacg tccgggtcca gggcgccctc ggcgaggccc tcctcgccct gaggaggtg 3540
cggtgggggg aggaggctgt aggccggccgc gtgggtccgg gcctacctcc tgcccgaccg 3600
ggaggtcctt ctccaggccg gccaggccgg ggaggcccaag gaggcggtgc cttcttaggg 3660
gttggccgt gagacctacg gccatcgatc tcgccccggg caaggaggcc tggcccccac 3720

ccctttgg

<210> 87
 <211> 1245
 <212> PRT
 <213> *Thermus thermophilus*

<400> 87
 Met Gly Arg Glu Leu Arg Phe Ala His Leu His Gln His Thr Gln Phe
 1 5 10 15
 Ser Leu Leu Asp Gly Ala Pro Lys Leu Ser Asp Leu Leu Lys Trp Val
 20 25 30
 Glu Glu Thr Thr Pro Glu Asp Pro Ala Leu Ala Met Thr Asp His Gly
 35 40 45
 Asn Leu Phe Gly Ala Val Glu Phe Tyr Lys Lys Ala Thr Glu Met Gly
 50 55 60
 Ile Lys Pro Ile Leu Gly Tyr Glu Ala Tyr Val Ala Ala Glu Ser Arg
 65 70 75 80
 Phe Asp Arg Lys Arg Gly Lys Gly Leu Asp Gly Gly Tyr Phe His Leu
 85 90 95
 Thr Leu Leu Ala Lys Asp Phe Thr Gly Tyr Gln Asn Leu Val Arg Leu
 100 105 110
 Ala Ser Arg Ala Tyr Leu Glu Gly Phe Tyr Glu Lys Pro Arg Ile Asp
 115 120 125
 Arg Glu Ile Leu Arg Glu His Ala Glu Gly Leu Ile Ala Leu Ser Gly
 130 135 140
 Cys Leu Gly Ala Glu Ile Pro Gln Phe Ile Leu Gln Asp Arg Leu Asp
 145 150 155 160
 Leu Ala Glu Ala Arg Leu Asn Glu Tyr Leu Ser Ile Phe Lys Asp Arg
 165 170 175
 Phe Phe Ile Glu Ile Gln Asn His Gly Leu Pro Glu Gln Lys Lys Val
 180 185 190
 Asn Glu Val Leu Lys Glu Phe Ala Arg Lys Tyr Gly Leu Gly Met Val
 195 200 205

Ala Thr Asn Asp Gly His Tyr Val Arg Lys Glu Asp Ala Arg Ala His
 210 215 220

Glu Val Leu Leu Ala Ile Gln Ser Lys Ser Thr Leu Asp Asp Pro Gly
 225 230 235 240

Ala Leu Ala Leu Pro Cys Glu Glu Phe Tyr Val Lys Thr Pro Glu Glu
 245 250 255

Met Arg Ala Met Phe Pro Glu Glu Val Gly Gly Arg Ser Pro Leu
 260 265 270

Thr Thr Pro Trp Arg Ser Pro His Val Gln Arg Gly Ala Ala Ile Gly
 275 280 285

Thr Arg Trp Ser Thr Arg Ile Pro Arg Phe Pro Leu Pro Glu Gly Arg
 290 295 300

Thr Glu Ala Gln Tyr Leu Met Glu Leu Thr Phe Lys Gly Leu Leu Arg
 305 310 315 320

Arg Tyr Pro Asp Arg Ile Thr Glu Gly Phe Tyr Arg Glu Val Phe Arg
 325 330 335

Leu Ser Gly Lys Leu Pro Pro His Gly Asp Gly Glu Ala Leu Ala Glu
 340 345 350

Ala Leu Ala Gln Val Glu Arg Glu Ala Trp Glu Arg Leu Met Lys Ser
 355 360 365

Leu Pro Pro Leu Ala Gly Val Lys Glu Trp Thr Ala Glu Ala Ile Phe
 370 375 380

His Arg Ala Leu Tyr Glu Leu Ser Ala Ile Glu Arg Met Gly Phe Pro
 385 390 395 400

Gly Leu Leu Pro His Arg Pro Gly Leu His Gln Leu Gly Pro Glu Lys
 405 410 415

Gly Val Ser Val Gly Pro Gly Arg Gly Gly Ala Ala Gly Ser Leu Val
 420 425 430

Ala Tyr Ala Val Gly Ile Thr Asn Ile Asp Pro Leu Arg Phe Gly Leu
 435 440 445

Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp Ile
 450 455 460

Asp	Thr	Asp	Phe	Ser	Asp	Arg	Glu	Arg	Asp	Arg	Val	Ile	Gln	Tyr	Val
465															480
Arg Glu Arg Tyr Gly Glu Asp Lys Val Ala Gln Ile Gly Thr Leu Gly															
															485 490 495
Ser	Leu	Ala	Ser	Lys	Ala	Ala	Leu	Lys	Glu	Val	Ala	Arg	Val	Tyr	Gly
															500 505 510
Ile	Pro	Arg	Lys	Lys	Ala	Glu	Glu	Leu	Ala	Lys	Leu	Ile	Pro	Val	Gln
															515 520 525
Phe	Gly	Lys	Pro	Lys	Pro	Leu	Gln	Glu	Ala	Ile	Gln	Val	Val	Pro	Glu
															530 535 540
Leu	Arg	Ala	Glu	Met	Glu	Lys	Asp	Pro	Lys	Val	Arg	Glu	Val	Leu	Glu
															545 550 555 560
Val	Ala	Met	Arg	Leu	Glu	Gly	Leu	Asn	Arg	His	Ala	Ser	Val.	His	Ala
															565 570 575
Gly	Arg	Gly	Gly	Val	Phe	Ser	Glu	Pro	Leu	Thr	Asp	Leu	Val	Pro	Leu
															580 585 590
Cys	Ala	Thr	Arg	Lys	Gly	Gly	Pro	Tyr	Thr	Gln	Tyr	Asp	Met	Gly	Ala
															595 600 605
Val	Glu	Ala	Leu	Gly	Leu	Leu	Lys	Met	Asp	Phe	Leu	Gly	Leu	Arg	Thr
															610 615 620
Leu	Thr	Phe	Leu	Asp	Glu	Val	Lys	Arg	Ile	Val	Lys	Ala	Ser	Gln	Gly
															625 630 635 640
Val	Glu	Leu	Asp	Tyr	Asp	Ala	Leu	Pro	Leu	Asp	Asp	Pro	Lys	Thr	Phe
															645 650 655
Ala	Leu	Leu	Ser	Arg	Gly	Glu	Thr	Lys	Gly	Val	Phe	Gln	Leu	Glu	Ser
															660 665 670
Gly	Gly	Met	Thr	Ala	Thr	Leu	Arg	Gly	Leu	Lys	Pro	Arg	Arg	Phe	Glu
															675 680 685
Asp	Leu	Ile	Ala	Ile	Leu	Ser	Leu	Tyr	Arg	Pro	Gly	Pro	Met	Glu	His
															690 695 700
Ile	Pro	Thr	Tyr	Ile	Arg	Arg	His	His	Gly	Leu	Glu	Pro	Val	Ser	Tyr
															705 710 715 720

Ser Glu Phe Pro His Ala Glu Lys Tyr Leu Lys Pro Ile Leu Asp Glu
725 730 735

Thr Tyr Gly Ile Pro Val Tyr Gln Glu Gln Ile Met Gln Ile Ala Ser
740 745 750

Ala Val Ala Gly Tyr Ser Leu Gly Glu Ala Asp Leu Leu Arg Arg Ser
755 760 765

Met Gly Lys Lys Val Glu Glu Met Lys Ser His Arg Glu Arg Phe
770 775 780

Val Gln Gly Ala Lys Glu Arg Gly Val Pro Glu Glu Ala Asn Arg
785 790 795 800

Leu Phe Asp Met Leu Glu Ala Phe Ala Asn Tyr Gly Phe Asn Lys Ser
805 810 815

His Ala Ala Ala Tyr Ser Leu Leu Ser Tyr Gln Thr Ala Tyr Val Lys
820 825 830

Ala His Tyr Pro Val Glu Phe Met Ala Ala Leu Leu Ser Val Glu Arg
835 840 845

His Asp Ser Asp Lys Val Ala Glu Tyr Ile Arg Asp Ala Arg Ala Met
850 855 860

Gly Ile Glu Val Leu Pro Pro Asp Val Asn Arg Ser Gly Phe Asp Phe
865 870 875 880

Leu Val Gln Gly Arg Gln Ile Leu Phe Gly Leu Ser Ala Val Lys Asn
885 890 895

Val Gly Glu Ala Ala Ala Glu Ala Ile Leu Arg Glu Arg Glu Arg Gly
900 905 910

Gly Pro Tyr Arg Ser Leu Gly Asp Phe Leu Lys Arg Leu Asp Glu Lys
915 920 925

Val Leu Asn Lys Arg Thr Leu Glu Ser Leu Ile Lys Ala Gly Ala Leu
930 935 940

Asp Gly Phe Gly Glu Arg Ala Arg Leu Leu Ala Ser Leu Glu Gly Leu
945 950 955 960

Leu Lys Trp Ala Ala Glu Asn Arg Glu Lys Ala Arg Ser Gly Met Met
965 970 975

Gly	Leu	Phe	Ser	Glu	Val	Glu	Glu	Pro	Pro	Leu	Ala	Glu	Ala	Ala	Pro
980						985						990			
Leu	Asp	Glu	Ile	Thr	Arg	Leu	Arg	Tyr	Glu	Lys	Glu	Ala	Leu	Gly	Ile
995						1000						1005			
Tyr	Val	Ser	Gly	His	Pro	Ile	Leu	Arg	Tyr	Pro	Gly	Leu	Arg	Glu	Thr
1010						1015						1020			
Ala	Thr	Cys	Thr	Leu	Glu	Glu	Leu	Pro	His	Leu	Ala	Arg	Asp	Leu	Pro
1025						1030						1035			1040
Pro	Arg	Ser	Arg	Val	Leu	Leu	Ala	Gly	Met	Val	Glu	Glu	Val	Val	Arg
											1045			1055	
Lys	Pro	Thr	Lys	Ser	Gly	Gly	Met	Met	Ala	Arg	Phe	Val	Leu	Ser	Asp
											1060			1070	
Glu	Thr	Gly	Ala	Leu	Glu	Ala	Val	Ala	Phe	Gly	Arg	Ala	Tyr	Asp	Gln
											1075			1085	
Val	Ser	Pro	Arg	Leu	Lys	Glu	Asp	Thr	Pro	Val	Leu	Val	Leu	Ala	Glu
											1090			1100	
Val	Glu	Arg	Glu	Glu	Gly	Gly	Val	Arg	Val	Leu	Ala	Gln	Ala	Val	Trp
											1105			1120	
Thr	Tyr	Gln	Glu	Leu	Glu	Gln	Val	Pro	Arg	Ala	Leu	Glu	Val	Glu	Val
											1125			1135	
Glu	Ala	Ser	Leu	Pro	Asp	Asp	Arg	Gly	Val	Ala	His	Leu	Lys	Ser	Leu
											1140			1150	
Leu	Asp	Glu	His	Ala	Gly	Thr	Leu	Pro	Leu	Tyr	Val	Arg	Val	Gln	Gly
											1155			1165	
Ala	Phe	Gly	Glu	Ala	Leu	Leu	Ala	Leu	Arg	Glu	Val	Arg	Val	Gly	Glu
											1170			1180	
Glu	Ala	Leu	Gly	Ala	Leu	Glu	Ala	Ala	Gly	Phe	Pro	Ala	Tyr	Leu	Leu
											1185			1200	
Pro	Asn	Arg	Glu	Val	Ser	Pro	Arg	Leu	Thr	Gly	Ser	Gly	Gly	Pro	Arg
											1205			1215	
Gly	Arg	Ala	Leu	Ser	Thr	Gly	Leu	Ala	Leu	Lys	Thr	Tyr	Pro	Ile	Ala
											1220			1230	

Leu Pro Gly Gly Asn Glu Ala Leu Ala Arg Pro Leu Leu
1235 1240 1245

<210> 88
<211> 198
<212> PRT
<213> Thermus thermophilus

<400> 88
Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu Glu
1 5 10 15

Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu Gly
20 25 30

Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly Leu
35 40 45

Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Arg Arg
50 55 60

Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala Arg
65 70 75 80

Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala Pro
85 90 95

Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp Ala
100 105 110

Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg Pro
115 120 125

Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp Ser
130 135 140

Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly Leu
145 150 155 160

Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His Arg
165 170 175

Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val Tyr
180 185 190

Tyr Met Leu Thr Ser Gly
195

<210> 89
<211> 182
<212> PRT
<213> Deinococcus radiodurans

<220>
<221> PEPTIDE
<222> (79)
<223> X at position 79 is undefined

<400> 89
Pro Trp Pro Gln Asp Val Val Val Phe Asp Leu Glu Thr Thr Gly Phe
1 5 10 15
Ser Pro Ala Ser Ala Ala Ile Val Glu Ile Gly Ala Val Arg Ile Val
20 25 30
Gly Gly Gln Ile Asp Glu Thr Leu Lys Phe Glu Thr Leu Val Arg Pro
35 40 45
Thr Arg Pro Asp Gly Ser Met Leu Ser Ile Pro Trp Gln Ala Gln Arg
50 55 60
Val His Gly Ile Ser Asp Glu Met Val Arg Arg Ala Pro Ala Xaa Lys
65 70 75 80
Asp Val Leu Pro Asp Phe Phe Asp Phe Val Asp Gly Ser Ala Val Val
85 90 95
Ala His Asn Val Ser Phe Asp Gly Gly Phe Met Arg Ala Gly Ala Glu
100 105 110
Arg Leu Gly Leu Ser Trp Ala Pro Glu Arg Glu Leu Cys Thr Met Gln
115 120 125
Leu Ser Arg Arg Ala Phe Pro Arg Glu Arg Thr His Asn Leu Thr Val
130 135 140
Leu Ala Glu Arg Leu Gly Leu Glu Phe Ala Pro Gly Gly Arg His Arg
145 150 155 160
Ser Tyr Gly Asp Val Gln Val Thr Ala Gln Ala Tyr Leu Arg Leu Leu
165 170 175
Glu Leu Leu Gly Glu Arg
180

<210> 90
<211> 201
<212> PRT
<213> *Bacillus subtilis*

<400> 90
His Gly Ile Lys Met Ile Tyr Gly Met Glu Ala Asn Leu Val Asp Asp
1 5 10 15
Gly Val Pro Ile Ala Tyr Asn Ala Ala His Arg Leu Leu Glu Glu Glu
20 25 30
Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val Tyr
35 40 45
Asp Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Gly Gly Glu Ile
50 55 60
Ile Asp Lys Phe Glu Ala Phe Ala Asn Pro His Arg Pro Leu Ser Ala
65 70 75 80
Thr Ile Ile Glu Leu Thr Gly Ile Thr Asp Asp Met Leu Gln Asp Ala
85 90 95
Pro Asp Val Val Asp Val Ile Arg Asp Phe Arg Glu Trp Ile Gly Asp
100 105 110
Asp Ile Leu Val Ala His Asn Ala Ser Phe Asp Met Gly Phe Leu Asn
115 120 125
Val Ala Tyr Lys Lys Leu Leu Glu Val Glu Lys Ala Lys Asn Pro Val
130 135 140
Ile Asp Thr Leu Glu Leu Gly Arg Phe Leu Tyr Pro Glu Phe Lys Asn
145 150 155 160
His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
165 170 175
His His Arg Ala Ile Tyr Asp Thr Glu Ala Thr Ala Tyr Leu Leu Leu
180 185 190
Lys Met Leu Lys Asp Ala Ala Glu Lys
195 200

<210> 91
<211> 188
<212> PRT
<213> Haemophilus influenzae

<220>
<221> PEPTIDE
<222> (47)
<223> X at position 47 is undefined

<220>
<221> PEPTIDE
<222> (57)
<223> X at position 57 is undefined

<400> 91
Met Ile Asn Pro Asn Arg Gln Ile Val Leu Asp Thr Glu Thr Thr Gly
1 5 10 15

Met Asn Gln Leu Gly Ala His Tyr Glu Gly His Cys Ile Ile Glu Ile
20 25 30

Gly Ala Val Glu Leu Ile Asn Arg Arg Tyr Thr Gly Asn Asn Xaa His
35 40 45

Ile Tyr Ile Lys Pro Asp Arg Pro Xaa Asp Pro Asp Ala Ile Lys Val
50 55 60

His Gly Ile Thr Asp Glu Met Leu Ala Asp Lys Pro Glu Phe Lys Glu
65 70 75 80

Val Ala Gln Asp Phe Leu Asp Tyr Ile Asn Gly Ala Glu Leu Leu Ile
85 90 95

His Asn Ala Pro Phe Asp Val Gly Phe Met Asp Tyr Glu Phe Arg Lys
100 105 110

Leu Asn Leu Asn Val Lys Thr Asp Asp Ile Cys Leu Val Thr Asp Thr
115 120 125

Leu Gln Met Ala Arg Gln Met Tyr Pro Gly Lys Arg Asn Asn Leu Asp
130 135 140

Ala Leu Cys Asp Arg Leu Gly Ile Asp Asn Ser Lys Arg Thr Leu His
145 150 155 160

Gly Ala Leu Leu Asp Ala Glu Ile Leu Ala Asp Val Tyr Leu Met Met
165 170 175

Thr Gly Gly Gln Thr Asn Leu Phe Asp Glu Glu Glu
180 185

<210> 92
<211> 189
<212> PRT
<213> Escherichia coli

<400> 92
Met Ser Thr Ala Ile Thr Arg Gln Ile Val Leu Asp Thr Glu Thr Thr
1 5 10 15

Gly Met Asn Gln Ile Gly Ala His Ser Glu Gly His Lys Ile Ile Glu
20 25 30

Ile Gly Ala Val Glu Val Val Asn Arg Arg Leu Thr Gly Asn Asn Phe
35 40 45

His Val Tyr Leu Lys Asp Arg Leu Val Asp Pro Glu Ala Phe Gly Val
50 55 60

His Gly Ile Ala Val Asp Phe Leu Leu Asp Lys Pro Thr Phe Ala Glu
65 70 75 80

Val Ala Val Glu Phe Met Asp Tyr Ile Arg Gly Ala Glu Leu Val Ile
85 90 95

His Asn Ala Ala Phe Asp Ile Gly Phe Met Asp Tyr Glu Phe Ser Leu
100 105 110

Leu Lys Arg Asp Ile Ala Lys Thr Asn Thr Phe Cys Lys Val Thr Asp
115 120 125

Ser Leu Ala Val Ala Arg Lys Met Phe Pro Gly Lys Arg Asn Ser Leu
130 135 140

Asp Ala Leu Cys Ala Arg Tyr Glu Ile Asp Asn Ser Lys Arg Thr Leu
145 150 155 160

His Gly Ala Leu Leu Asp Ala Gln Ile Leu Ala Glu Val Tyr Leu Ala
165 170 175

Met Thr Gly Gly Gln Thr Ser Met Ala Phe Ala Met Glu
180 185

<210> 93
<211> 201
<212> PRT
<213> Helicobacter pylori

<400> 93
Asn Leu Glu Tyr Leu Lys Ala Cys Gly Leu Asn Phe Ile Glu Thr Ser
1 5 10 15

Glu Asn Leu Ile Thr Leu Lys Asn Leu Lys Thr Pro Leu Lys Asp Glu
20 25 30

Val Phe Ser Phe Ile Asp Leu Glu Thr Thr Gly Ser Cys Pro Ile Lys
35 40 45

His Glu Ile Leu Glu Ile Gly Ala Val Gln Val Lys Gly Gly Glu Ile
50 55 60

Ile Asn Arg Phe Glu Thr Leu Val Lys Val Lys Ser Val Pro Asp Tyr
65 70 75 80

Ile Ala Glu Leu Thr Gly Ile Thr Tyr Glu Asp Thr Leu Asn Ala Pro
85 90 95

Ser Ala His Glu Ala Leu Gln Glu Leu Arg Leu Phe Leu Gly Asn Ser
100 105 110

Val Phe Val Ala His Asn Ala Asn Phe Asp Tyr Asn Phe Leu Gly Arg
115 120 125

Tyr Phe Val Glu Lys Leu His Cys Pro Leu Leu Asn Leu Lys Leu Cys
130 135 140

Thr Leu Asp Leu Ser Lys Arg Ala Ile Leu Ser Met Arg Tyr Ser Leu
145 150 155 160

Ser Phe Leu Lys Glu Leu Leu Gly Phe Gly Ile Glu Val Ser His Arg
165 170 175

Ala Tyr Ala Asp Ala Leu Ala Ser Tyr Lys Leu Phe Glu Ile Cys Leu
180 185 190

Leu Asn Leu Pro Ser Tyr Ile Lys Thr
195 200

<210> 94
<211> 630

<212> DNA

<213> Thermus thermophilus

<400> 94

atgggtggagc ggggtggtgcg gacccttctg gacgggaggt tcctcctgga ggaggggggtg 60
gggcttggg agtggcgcta ccccttccc ctggaggggg aggcggtgt ggtcctggac 120
ctggagacca cggggcttgc cggcctggac gaggtgattg aggtgggcct cctccgcctg 180
gagggggggga ggccgcctccc ctccagagc ctcgtccggc ccctcccgcc cgccgaagcc 240
cgttcgtgga acctcaccgg catccccgg gaggccctgg aggaggccccc ctccctggag 300
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gccttgcacc tgggcttccct ccggccggcc ttggagggcc tgggctaccg cctggaaaac 420
cccggtgtgg actccctgca cttggccaga cggggcttac caggccttag ggcgtacggc 480
ctggacgcacc tctccgaggt cttggagctt ccccgaaagga cctgccaccg ggccctcgag 540
gacgtggagc gcaccctcgc cgtggtgcac gaggtatact atatgcttac gtccggccgt 600
ccccgcacgc tttggaaact cgggaggtag 630

<210> 95

<211> 210

<212> PRT

<213> Thermus thermophilus

<400> 95

Met Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu
1 5 10 15

Glu Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu
20 25 30

Gly Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly
35 40 45

Leu Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg
50 55 60

Arg Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala
65 70 75 80

Arg Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala
85 90 95

Pro Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp
100 105 110

Ala Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg
115 120 125

Pro Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp

130	135	140
Ser Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly		
145	150	160
Leu Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His		
165	170	175
Arg Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val		
180	185	190
Tyr Tyr Met Leu Thr Ser Gly Arg Pro Arg Thr Leu Trp Glu Leu Gly		
195	200	205
Arg Glx		
210		
<210> 96		
<211> 461		
<212> PRT		
<213> Pseudomonas marcesans		
<400> 96		
Met Leu Glu Ala Ser Trp Glu Lys Val Gln Ser Ser Leu Lys Gln Asn		
1	5	10
		15
Leu Ser Lys Pro Ser Tyr Glu Thr Trp Ile Arg Pro Thr Glu Phe Ser		
20	25	30
Gly Phe Lys Asn Gly Glu Leu Thr Leu Ile Ala Pro Asn Ser Phe Ser		
35	40	45
Ser Ala Trp Leu Lys Asn Asn Tyr Ser Gln Thr Ile Gln Glu Thr Ala		
50	55	60
Glu Glu Ile Phe Gly Glu Pro Val Thr Val His Val Lys Val Lys Ala		
65	70	75
		80
Asn Ala Glu Ser Ser Asp Glu His Tyr Ser Ser Ala Pro Ile Thr Pro		
85	90	95
Pro Leu Glu Ala Ser Pro Gly Ser Val Asp Ser Ser Gly Ser Ser Leu		
100	105	110
Arg Leu Ser Lys Lys Thr Leu Pro Leu Leu Asn Leu Arg Tyr Val Phe		
115	120	125

Asn	Arg	Phe	Val	Val	Gly	Pro	Asn	Ser	Arg	Met	Ala	His	Ala	Ala	Ala
130															
Met	Ala	Val	Ala	Glu	Ser	Pro	Gly	Arg	Glu	Phe	Asn	Pro	Leu	Phe	Ile
145															
Cys	Gly	Gly	Val	Gly	Leu	Gly	Lys	Thr	His	Leu	Met	Gln	Ala	Ile	Gly
165															175
His	Tyr	Arg	Leu	Glu	Ile	Asp	Pro	Gly	Ala	Lys	Val	Ser	Tyr	Val	Ser
180															190
Thr	Glu	Thr	Phe	Thr	Asn	Asp	Leu	Ile	Leu	Ala	Ile	Arg	Gln	Asp	Arg
195															205
Met	Gln	Ala	Phe	Arg	Asp	Arg	Tyr	Arg	Ala	Ala	Asp	Leu	Ile	Leu	Val
210															220
Asp	Asp	Ile	Gln	Phe	Ile	Glu	Gly	Lys	Glu	Tyr	Thr	Gln	Glu	Glu	Phe
225															240
Phe	His	Thr	Phe	Asn	Ala	Leu	His	Asp	Ala	Gly	Ser	Gln	Ile	Val	Leu
245															255
Ala	Ser	Asp	Arg	Pro	Pro	Ser	Gln	Ile	Pro	Arg	Leu	Gln	Glu	Arg	Leu
260															270
Met	Ser	Arg	Phe	Ser	Met	Gly	Leu	Ile	Ala	Asp	Val	Gln	Ala	Pro	Asp
275															285
Leu	Glu	Thr	Arg	Met	Ala	Ile	Leu	Gln	Lys	Lys	Ala	Glu	His	Glu	Arg
290															300
Val	Gly	Leu	Pro	Arg	Asp	Leu	Ile	Gln	Phe	Ile	Ala	Gly	Arg	Phe	Thr
305															320
Ser	Asn	Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Thr	Arg	Ala	Ile	Ala	Phe
325															335
Ala	Ser	Ile	Thr	Gly	Leu	Pro	Met	Thr	Val	Asp	Ser	Ile	Ala	Pro	Met
340															350
Leu	Asp	Pro	Asn	Gly	Gln	Gly	Val	Glu	Val	Thr	Pro	Lys	Gln	Val	Leu
355															365
Asp	Lys	Val	Ala	Glu	Val	Phe	Lys	Val	Thr	Pro	Asp	Glu	Met	Arg	Ser
370															380

Ala Ser Arg Arg Arg Pro Val Ser Gln Ala Arg Gln Val Gly Met Tyr
385 390 395 400

Leu Met Arg Gln Gly Thr Asn Leu Ser Leu Pro Arg Ile Gly Asp Thr
405 410 415

Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ala Ile Glu Gln Val
420 425 430

Glu Lys Lys Leu Ser Ser Asp Pro Gln Ile Ala Ser Gln Val Gln Lys
435 440 445

Ile Arg Asp Leu Leu Gln Ile Asp Ser Arg Arg Lys Arg
450 455 460

<210> 97

<211> 447

<212> PRT

<213> Synechocystis sp.

<400> 97

Met Val Ser Cys Glu Asn Leu Trp Gln Gln Ala Leu Ala Ile Leu Ala
1 5 10 15

Thr Gln Leu Thr Lys Pro Ala Phe Asp Thr Trp Ile Lys Ala Ser Val
20 25 30

Leu Ile Ser Leu Gly Asp Gly Val Ala Thr Ile Gin Val Glu Asn Gly
35 40 45

Phe Val Leu Asn His Leu Gln Lys Ser Tyr Gly Pro Leu Leu Met Glu
50 55 60

Val Leu Thr Asp Leu Thr Gly Gln Glu Ile Thr Val Lys Leu Ile Thr
65 70 75 80

Asp Gly Leu Glu Pro His Ser Leu Ile Gly Gln Glu Ser Ser Leu Pro
85 90 95

Met Glu Thr Thr Pro Lys Asn Ala Thr Ala Leu Asn Gly Lys Tyr Thr
100 105 110

Phe Ser Arg Phe Val Val Gly Pro Thr Asn Arg Met Ala His Ala Ala
115 120 125

Ser Leu Ala Val Ala Glu Ser Pro Gly Arg Glu Phe Asn Pro Leu Phe
130 135 140

Leu Cys Gly Gly Val Gly Leu Gly Lys Thr His Leu Met Gln Ala Ile
 145 150 155 160
 Ala His Tyr Arg Leu Glu Met Tyr Pro Asn Ala Lys Val Tyr Tyr Val
 165 170 175
 Ser Thr Glu Arg Phe Thr Asn Asp Leu Ile Thr Ala Ile Arg Gln Asp
 180 185 190
 Asn Met Glu Asp Phe Arg Ser Tyr Tyr Arg Ser Ala Asp Phe Leu Leu
 195 200 205
 Ile Asp Asp Ile Gln Phe Ile Lys Gly Lys Glu Tyr Thr Gln Glu Glu
 210 215 220
 Phe Phe His Thr Phe Asn Ser Leu His Glu Ala Gly Lys Gln Val Val
 225 230 235 240
 Val Ala Ser Asp Arg Ala Pro Gln Arg Ile Pro Gly Leu Gln Asp Arg
 245 250 255
 Leu Ile Ser Arg Phe Ser Met Gly Leu Ile Ala Asp Ile Gln Val Pro
 260 265 270
 Asp Leu Glu Thr Arg Met Ala Ile Leu Gln Lys Lys Ala Glu Tyr Asp
 275 280 285
 Arg Ile Arg Leu Pro Lys Glu Val Ile Glu Tyr Ile Ala Ser His Tyr
 290 295 300
 Thr Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Ile Arg Ala Ile Ala
 305 310 315 320
 Tyr Thr Ser Leu Ser Asn Val Ala Met Thr Val Glu Asn Ile Ala Pro
 325 330 335
 Val Leu Asn Pro Pro Val Glu Lys Val Ala Ala Ala Pro Glu Thr Ile
 340 345 350
 Ile Thr Ile Val Ala Gln His Tyr Gln Leu Lys Val Glu Glu Leu Leu
 355 360 365
 Ser Asn Ser Arg Arg Arg Glu Val Ser Leu Ala Arg Gln Val Gly Met
 370 375 380
 Tyr Leu Met Arg Gln His Thr Asp Leu Ser Leu Pro Arg Ile Gly Glu
 385 390 395 400

Ala Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ser Cys Asp Lys
405 410 415

Ile Thr Gln Leu Gln Gln Lys Asp Trp Glu Thr Ser Gln Thr Leu Thr
420 425 430

Ser Leu Ser His Arg Ile Asn Ile Ala Gly Gln Ala Pro Glu Ser
435 440 445

<210> 98

<211> 446

<212> PRT

<213> *Bacillus subtilis*

<400> 98
Met Glu Asn Ile Leu Asp Leu Trp Asn Gln Ala Leu Ala Gln Ile Glu
1 5 10 15

Lys Lys Leu Ser Lys Pro Ser Phe Glu Thr Trp Met Lys Ser Thr Lys
20 25 30

Ala His Ser Leu Gln Gly Asp Thr Leu Thr Ile Thr Ala Pro Asn Glu
35 40 45

Phe Ala Arg Asp Trp Leu Glu Ser Arg Tyr Leu His Leu Ile Ala Asp
50 55 60

Thr Ile Tyr Glu Leu Thr Gly Glu Glu Leu Ser Ile Lys Phe Val Ile
65 70 75 80

Pro Gln Asn Gln Asp Val Glu Asp Phe Met Pro Lys Pro Gln Val Lys
85 90 95

Lys Ala Val Lys Glu Asp Thr Ser Asp Phe Pro Gln Asn Met Leu Asn
100 105 110

Pro Lys Tyr Thr Phe Asp Thr Phe Val Ile Gly Ser Gly Asn Arg Phe
115 120 125

Ala His Ala Ala Ser Leu Ala Val Ala Glu Ala Pro Ala Lys Ala Tyr
130 135 140

Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr His Leu
145 150 155 160

Met His Ala Ile Gly His Tyr Val Ile Asp His Asn Pro Ser Ala Lys

165

170

175

Val Val Tyr Leu Ser Ser Glu Lys Phe Thr Asn Glu Phe Ile Asn Ser
 180 185 190

Ile Arg Asp Asn Lys Ala Val Asp Phe Arg Asn Arg Tyr Arg Asn Val
 195 200 205

Asp Val Leu Leu Ile Asp Asp Ile Gln Phe Leu Ala Gly Lys Glu Gln
 210 215 220

Thr Gln Glu Glu Phe Phe His Thr Phe Asn Thr Leu His Glu Glu Ser
 225 230 235 240

Lys Gln Ile Val Ile Ser Ser Asp Arg Pro Pro Lys Glu Ile Pro Thr
 245 250 255

Leu Glu Asp Arg Leu Arg Ser Arg Phe Glu Trp Gly Leu Ile Thr Asp
 260 265 270

Ile Thr Pro Pro Asp Leu Glu Thr Arg Ile Ala Ile Leu Arg Lys Lys
 275 280 285

Ala Lys Ala Glu Gly Leu Asp Ile Pro Asn Glu Val Met Leu Tyr Ile
 290 295 300

Ala Asn Gln Ile Asp Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Ile
 305 310 315 320

Arg Val Val Ala Tyr Ser Ser Leu Ile Asn Lys Asp Ile Asn Ala Asp
 325 330 335

Leu Ala Ala Glu Ala Leu Lys Asp Ile Ile Pro Ser Ser Lys Pro Lys
 340 345 350

Val Ile Thr Ile Lys Glu Ile Gln Arg Val Val Gly Gln Gln Phe Asn
 355 360 365

Ile Lys Leu Glu Asp Phe Lys Ala Lys Lys Arg Thr Lys Ser Val Ala
 370 375 380

Phe Pro Arg Gln Ile Ala Met Tyr Leu Ser Arg Glu Met Thr Asp Ser
 385 390 395 400

Ser Leu Pro Lys Ile Gly Glu Glu Phe Gly Gly Arg Asp His Thr Thr
 405 410 415

Val Ile His Ala His Glu Lys Ile Ser Lys Leu Leu Ala Asp Asp Glu

420

425

430

Gln Leu Gln Gln His Val Lys Glu Ile Lys Glu Gln Leu Lys
 435 440 445

<210> 99
 <211> 507
 <212> PRT
 <213> *Mycobacterium tuberculosis*

<400> 99
 Met Thr Asp Asp Pro Gly Ser Gly Phe Thr Thr Val Trp Asn Ala Val
 1 5 10 15
 Val Ser Glu Leu Asn Gly Asp Pro Lys Val Asp Asp Gly Pro Ser Ser
 20 25 30
 Asp Ala Asn Leu Ser Ala Pro Leu Thr Pro Gln Gln Arg Ala Trp Leu
 35 40 45
 Asn Leu Val Gln Pro Leu Thr Ile Val Glu Gly Phe Ala Leu Leu Ser
 50 55 60
 Val Pro Ser Ser Phe Val Gln Asn Glu Ile Glu Arg His Leu Arg Ala
 65 70 75 80
 Pro Ile Thr Asp Ala Leu Ser Arg Arg Leu Gly His Gln Ile Gln Leu
 85 90 95
 Gly Val Arg Ile Ala Pro Pro Ala Thr Asp Glu Ala Asp Asp Thr Thr
 100 105 110
 Val Pro Pro Ser Glu Asn Pro Ala Thr Thr Ser Pro Asp Thr Thr Thr
 115 120 125
 Asp Asn Asp Glu Ile Asp Asp Ser Ala Ala Ala Arg Gly Asp Asn Gln
 130 135 140
 His Ser Trp Pro Ser Tyr Phe Thr Glu Arg Pro His Asn Thr Asp Ser
 145 150 155 160
 Ala Thr Ala Gly Val Thr Ser Leu Asn Arg Arg Tyr Thr Phe Asp Thr
 165 170 175
 Phe Val Ile Gly Ala Ser Asn Arg Phe Ala His Ala Ala Leu Ala
 180 185 190

Ile Ala Glu Ala Pro Ala Arg Ala Tyr Asn Pro Leu Phe Ile Trp Gly
 195 200 205
 Glu Ser Gly Leu Gly Lys Thr His Leu Leu His Ala Ala Gly Asn Tyr
 210 215 220
 Ala Gln Arg Leu Phe Pro Gly Met Arg Val Lys Tyr Val Ser Thr Glu
 225 230 235 240
 Glu Phe Thr Asn Asp Phe Ile Asn Ser Leu Arg Asp Asp Arg Lys Val
 245 250 255
 Ala Phe Lys Arg Ser Tyr Arg Asp Val Asp Val Leu Leu Val Asp Asp
 260 265 270
 Ile Gln Phe Ile Glu Gly Lys Glu Gly Ile Gln Glu Glu Phe Phe His
 275 280 285
 Thr Phe Asn Thr Leu His Asn Ala Asn Lys Gln Ile Val Ile Ser Ser
 290 295 300
 Asp Arg Pro Pro Lys Gln Leu Ala Thr Leu Glu Asp Arg Leu Arg Thr
 305 310 315 320
 Arg Phe Glu Trp Gly Leu Ile Thr Asp Val Gln Pro Pro Glu Leu Glu
 325 330 335
 Thr Arg Ile Ala Ile Leu Arg Lys Lys Ala Gln Met Glu Arg Leu Ala
 340 345 350
 Val Pro Asp Asp Val Leu Glu Leu Ile Ala Ser Ser Ile Glu Arg Asn
 355 360 365
 Ile Arg Glu Leu Glu Gly Ala Leu Ile Arg Val Thr Ala Phe Ala Ser
 370 375 380
 Leu Asn Lys Thr Pro Ile Asp Lys Ala Leu Ala Glu Ile Val Leu Arg
 385 390 395 400
 Asp Leu Ile Ala Asp Ala Asn Thr Met Gln Ile Ser Ala Ala Thr Ile
 405 410 415
 Met Ala Ala Thr Ala Glu Tyr Phe Asp Thr Thr Val Glu Glu Leu Arg
 420 425 430
 Gly Pro Gly Lys Thr Arg Ala Leu Ala Gln Ser Arg Gln Ile Ala Met
 435 440 445

Tyr Leu Cys Arg Glu Leu Thr Asp Leu Ser Leu Pro Lys Ile Gly Gln
450 455 460

Ala Phe Gly Arg Asp His Thr Thr Val Met Tyr Ala Gln Arg Lys Ile
465 470 475 480

Leu Ser Glu Met Ala Glu Arg Arg Glu Val Phe Asp His Val Lys Glu
485 490 495

Leu Thr Thr Arg Ile Arg Gln Arg Ser Lys Arg
500 505

<210> 100

<211> 446

<212> PRT

<213> *Thermus thermophilus*

<400> 100

Met Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
1 5 10 15

Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
20 25 30

Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
35 40 45

Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly
50 55 60

Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val
65 70 75 80

Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro
85 90 95

Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly
100 105 110

Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser
115 120 125

Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu
130 135 140

Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg
145 150 155 160

Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn
165 170 175

Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg
180 185 190

Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe
195 200 205

Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn
210 215 220

Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro
225 230 235 240

Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu
245 250 255

Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile
260 265 270

Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp
275 280 285

Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp
290 295 300

Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val
305 310 315 320

Glu Leu Thr Arg Ala Val' Ala Ala Lys Ala Leu Arg His Leu Arg Pro
325 330 335

Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly
340 345 350

Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys
355 360 365

Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu
370 375 380

Leu Thr Pro Ala Ser Leu Pro Glu Ile Gly Gln Leu Phe Gly Gly Arg
385 390 395 400

Asp His Thr Thr Val Arg Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala
405 410 415

Gly Lys Pro Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu
420 425 430

Ala Cys Thr Asp Pro Val Asp Asn Leu Trp Ile Thr Cys Gly
435 440 445

<210> 101

<211> 467

<212> PRT

<213> Escherichia coli

<400> 101

Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu
1 5 10 15

Leu Pro Ala Thr Glu Phe Ser Met Trp Ile Arg Pro Leu Gln Ala Glu
20 25 30

Leu Ser Asp Asn Thr Leu Ala Leu Tyr Ala Pro Asn Arg Phe Val Leu
35 40 45

Asp Trp Val Arg Asp Lys Tyr Leu Asn Asn Ile Asn Gly Leu Leu Thr
50 55 60

Ser Phe Cys Gly Ala Asp Ala Pro Gln Leu Arg Phe Glu Val Gly Thr
65 70 75 80

Lys Pro Val Thr Gln Thr Pro Gln Ala Ala Val Thr Ser Asn Val Ala
85 90 95

Ala Pro Ala Gln Val Ala Gln Thr Gln Pro Gln Arg Ala Ala Pro Ser
100 105 110

Thr Arg Ser Gly Trp Asp Asn Val Pro Ala Pro Ala Glu Pro Thr Tyr
115 120 125

Arg Ser Asn Val Asn Val Lys His Thr Phe Asp Asn Phe Val Glu Gly
130 135 140

Lys Ser Asn Gln Leu Ala Arg Ala Ala Arg Gln Val Ala Asp Asn
145 150 155 160

Pro Gly Gly Ala Tyr Asn Pro Leu Phe Leu Tyr Gly Gly Thr Gly Leu
165 170 175

Gly Lys Thr His Leu Leu His Ala Val Gly Asn Gly Ile Met Ala Arg

180	185	190
Lys Pro Asn Ala Lys Val Val Tyr Met His Ser Glu Arg Phe Val Gln		
195	200	205
Asp Met Val Lys Ala Leu Gln Asn Asn Ala Ile Glu Glu Phe Lys Arg		
210	215	220
Tyr Tyr Arg Ser Val Asp Ala Leu Leu Ile Asp Asp Ile Gln Phe Phe		
225	230	235
Ala Asn Lys Glu Arg Ser Gln Glu Glu Phe Phe His Thr Phe Asn Ala		
245	250	255
Leu Leu Glu Gly Asn Gln Gln Ile Ile Leu Thr Ser Asp Arg Tyr Pro		
260	265	270
Lys Glu Ile Asn Gly Val Glu Asp Arg Leu Lys Ser Arg Phe Gly Trp		
275	280	285
Gly Leu Thr Val Ala Ile Glu Pro Pro Glu Leu Glu Thr Arg Val Ala		
290	295	300
Ile Leu Met Lys Lys Ala Asp Glu Asn Asp Ile Arg Leu Pro Gly Glu		
305	310	315
Val Ala Phe Phe Ile Ala Lys Arg Leu Arg Ser Asn Val Arg Glu Leu		
325	330	335
Glu Gly Ala Leu Asn Arg Val Ile Ala Asn Ala Asn Phe Thr Gly Arg		
340	345	350
Ala Ile Thr Ile Asp Phe Val Arg Glu Ala Leu Arg Asp Leu Leu Ala		
355	360	365
Leu Gln Glu Lys Leu Val Thr Ile Asp Asn Ile Gln Lys Thr Val Ala		
370	375	380
Glu Tyr Tyr Lys Ile Lys Val Ala Asp Leu Leu Ser Lys Arg Arg Ser		
385	390	395
Arg Ser Val Ala Arg Pro Arg Gln Met Ala Met Ala Leu Ala Lys Glu		
405	410	415
Leu Thr Asn His Ser Leu Pro Glu Ile Gly Asp Ala Phe Gly Gly Arg		
420	425	430
Asp His Thr Thr Val Leu His Ala Cys Arg Lys Ile Glu Gln Leu Arg		

435

440

445

Glu Glu Ser His Asp Ile Lys Glu Asp Phe Ser Asn Leu Ile Arg Thr
 450 455 460

Leu Ser Ser
 465

<210> 102
 <211> 440
 <212> PRT
 <213> Thermatoga maritima

<400> 102
 Met Lys Glu Arg Ile Leu Gln Glu Ile Lys Thr Arg Val Asn Arg Lys
 1 5 10 15

Ser Trp Glu Leu Trp Phe Ser Ser Phe Asp Val Lys Ser Ile Glu Gly
 20 25 30

Asn Lys Val Val Phe Ser Val Gly Asn Leu Phe Ile Lys Glu Trp Leu
 35 40 45

Glu Lys Lys Tyr Tyr Ser Val Leu Ser Lys Ala Val Lys Val Val Leu
 50 55 60

Gly Asn Asp Ala Thr Phe Glu Ile Thr Tyr Glu Ala Phe Glu Pro His
 65 70 75 80

Ser Ser Tyr Ser Glu Pro Leu Val Lys Lys Arg Ala Val Leu Leu Thr
 85 90 95

Pro Leu Asn Pro Asp Tyr Thr Phe Glu Asn Phe Val Val Gly Pro Gly
 100 105 110

Asn Ser Phe Ala Tyr His Ala Ala Leu Glu Val Ala Lys His Pro Gly
 115 120 125

Arg Tyr Asn Pro Leu Phe Ile Tyr Gly Val Gly Leu Gly Lys Thr
 130 135 140

His Leu Leu Gln Ser Ile Gly Asn Tyr Val Val Gln Asn Glu Pro Asp
 145 150 155 160

Leu Arg Val Met Tyr Ile Thr Ser Glu Lys Phe Leu Asn Asp Leu Val
 165 170 175

Asp Ser Met Lys Glu Gly Lys Leu Asn Glu Phe Arg Glu Lys Tyr Arg
180 185 190

Lys Lys Val Asp Ile Leu Leu Ile Asp Asp Val Gln Phe Leu Ile Gly
195 200 205

Lys Thr Gly Val Gln Thr Glu Leu Phe His Thr Phe Asn Glu Leu His
210 215 220

Asp Ser Gly Lys Gln Ile Val Ile Cys Ser Asp Arg Glu Pro Gln Lys
225 230 235 240

Leu Ser Glu Phe Gln Asp Arg Leu Val Ser Arg Phe Gln Met Gly Leu
245 250 255

Val Ala Lys Leu Glu Pro Pro Asp Glu Glu Thr Arg Lys Ser Ile Ala
260 265 270

Arg Lys Met Leu Glu Ile Glu His Gly Glu Leu Pro Glu Glu Val Leu
275 280 285

Asn Phe Val Ala Glu Asn Val Asp Asp Asn Leu Arg Arg Leu Arg Gly
290 295 300

Ala Ile Ile Lys Leu Leu Val Tyr Lys Glu Thr Thr Gly Lys Glu Val
305 310 315 320

Asp Leu Lys Glu Ala Ile Leu Leu Lys Asp Phe Ile Lys Pro Asn
325 330 335

Arg Val Lys Ala Met Asp Pro Ile Asp Glu Leu Ile Glu Ile Val Ala
340 345 350

Lys Val Thr Gly Val Pro Arg Glu Glu Ile Leu Ser Asn Ser Arg Asn
355 360 365

Val Lys Ala Leu Thr Ala Arg Arg Ile Gly Met Tyr Val Ala Lys Asn
370 375 380

Tyr Leu Lys Ser Ser Leu Arg Thr Ile Ala Glu Lys Phe Asn Arg Ser
385 390 395 400

His Pro Val Val Val Asp Ser Val Lys Lys Val Lys Asp Ser Leu Leu
405 410 415

Lys Gly Asn Lys Gln Leu Lys Ala Leu Ile Asp Glu Val Ile Gly Glu
420 425 430

Ile Ser Arg Arg Ala Leu Ser Gly
435 440

<210> 103
<211> 457
<212> PRT
<213> Helicobacter pylori

<400> 103
Met Asp Thr Asn Asn Asn Ile Glu Lys Glu Ile Leu Ala Leu Val Lys
1 5 10 15
Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu Asn Tyr Phe Ser Gln
20 25 30
Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp Ile Ala Phe Phe Tyr
35 40 45
Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr Ala Lys Tyr Gly Ala
50 55 60
Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val Gly Met His Leu Ala
65 70 75 80
His Ser Val Asp Val Arg Ile Glu Val Ala Pro Lys Ile Gln Ile Asn
85 90 95
Ala Gln Ser Asn Ile Asn Tyr Lys Ala Ile Lys Thr Ser Val Lys Asp
100 105 110
Ser Tyr Thr Phe Glu Asn Phe Val Val Gly Ser Cys Asn Asn Thr Val
115 120 125
Tyr Glu Ile Ala Lys Lys Val Ala Gln Ser Asp Thr Pro Pro Tyr Asn
130 135 140
Pro Val Leu Phe Tyr Gly Thr Gly Leu Gly Lys Thr His Ile Leu
145 150 155 160
Asn Ala Ile Gly Asn His Ala Leu Glu Lys His Lys Lys Val Val Leu
165 170 175
Val Thr Ser Glu Asp Phe Leu Thr Asp Phe Leu Lys His Leu Asp Asn
180 185 190
Lys Thr Met Asp Ser Phe Lys Ala Lys Tyr Arg His Cys Asp Phe Phe
195 200 205

Leu Leu Asp Asp Ala Gln Phe Leu Gln Gly Lys Pro Lys Leu Glu Glu
210 215 220

Glu Phe Phe His Thr Phe Asn Glu Leu His Ala Asn Ser Lys Gln Ile
225 230 235 240

Val Leu Ile Ser Asp Arg Ser Pro Lys Asn Ile Ala Gly Leu Glu Asp
245 250 255

Arg Leu Lys Ser Arg Phe Glu Trp Gly Ile Thr Ala Lys Val Met Pro
260 265 270

Pro Asp Leu Glu Thr Lys Leu Ser Ile Val Lys Gln Lys Cys Gln Leu
275 280 285

Asn Gln Ile Thr Leu Pro Glu Glu Val Met Glu Tyr Ile Ala Gln His
290 295 300

Ile Ser Asp Asn Ile Arg Gln Met Glu Gly Ala Ile Ile Lys Ile Ser
305 310 315 320

Val Asn Ala Asn Leu Met Asn Ala Ser Ile Asp Leu Asn Leu Ala Lys
325 330 335

Thr Val Leu Glu Asp Leu Gln Lys Asp His Ala Glu Gly Ser Ser Leu
340 345 350

Glu Asn Ile Leu Leu Ala Val Ala Gln Ser Leu Asn Leu Lys Ser Ser
355 360 365

Glu Ile Lys Val Ser Ser Arg Gln Lys Asn Val Ala Leu Ala Arg Lys
370 375 380

Leu Val Val Tyr Phe Ala Arg Leu Tyr Thr Pro Asn Pro Thr Leu Ser
385 390 395 400

Leu Ala Gln Phe Leu Asp Leu Lys Asp His Ser Ser Ile Ser Lys Met
405 410 415

Tyr Ser Gly Val Lys Lys Met Leu Glu Glu Lys Ser Pro Phe Val
420 425 430

Leu Ser Leu Arg Glu Glu Ile Lys Asn Arg Leu Asn Glu Leu Asn Asp
435 440 445

Lys Lys Thr Ala Phe Asn Ser Ser Glu
450 455

<210> 104
<211> 1305
<212> DNA
<213> *Thermus thermophilus*

<400> 104
gtgtcgacg aggccgtctg gcaacacgtt ctggagcaca tccgcccgcag catcaccgag 60
gtgagttcc acacctggtt taaaaggatc cgcccccggg ggatccggga cgggggtgctg 120
gagctcgccg tgcccacctc cttgcctg gactggatcc ggcgcacta cgccggcctc 180
atccaggagg gcccctggct cctcggggcc caggcccccc gggtttagct ccgggtggtg 240
ccgggggtcg tagtccagga ggacatcttc cagccccgc cgagcccccc ggccaagct 300
caacccgaag ataccttaa aacttcgtgg tggggccaa caactccatg gccccacggc 360
ggccgcgtgg ccgtggccga gtcccccggc cggccctaca acccccttt catctacggg 420
ggccgtggcc tggaaagac ctacctgatg cacgcgtgg gcccactccg tgcgaagcgc 480
ttcccccaca tgagattaga gtacgtttcc acggaaactt tcaccaacga gctcatcaac 540
cgcccatccg cgagggaccg gatgacggag ttccgggagc ggtaccgctc cgtgaccc 600
ctgctggtgg acgacgtcca gttcatcgcc ggaaaggagc gcacccagga ggagtttttc 660
cacacccatca acgccccctta cgaggcccac aagcagatca tcctctcctc cgaccggccg 720
cccaaggaca tcctcaccct ggaggcgcgc ctgcgagcc gcttgagtg gggctgtatc 780
accgacaatc cagccccca cctggaaacc cggatcgcca tcctgaagat gaacgcccagc 840
agcgggcctg aggatcccga ggacgcctg gatgacatcg cccggcaggt cacctccaac 900
atccgggagt gggaaaggggc cctcatgcgg gcatgcctt tcgcctccct caacggcggt 960
gagctgaccc ggcgcgtggc ggcacaggct ctccgacatc ttccgccttggag 1020
gcggacccct tggagatcat cgcacccatc gcgggaccag ttccgcctga aacccggga 1080
ggagctcacg gggagcgcgc caagaaggag gtggcctcc cccggcagct cgccatgtac 1140
ctggcggcgg agctcacccccc ggcctccctg cccgagatcg accagctcaa cgacgaccgg 1200
gaccacacca cggcctctca cgccatccag aagggtccagg agctcgccga aagcgcacgg 1260
gaggtgcagg gcctccctccg caccctccgg gaggcgtgca catga 1305

<210> 105
<211> 434
<212> PRT
<213> *Thermus thermophilus*

<400> 105
Val Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
1 5 10 15
Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
20 25 30
Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
35 40 45
Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly

50	55	60
Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val		
65	70	75
Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro		
85	90	95
Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly		
100	105	110
Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser		
115	120	125
Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu		
130	135	140
Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg		
145	150	160
Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn		
165	170	175
Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg		
180	185	190
Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe		
195	200	205
Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn		
210	215	220
Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro		
225	230	235
Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu		
245	250	255
Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile		
260	265	270
Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp		
275	280	285
Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp		
290	295	300
Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val		

305	310	315	320
Glu Leu Thr Arg Ala Val Ala Ala Lys Ala Leu Arg His Leu Arg Pro			
325	330	335	
Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly			
340	345	350	
Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys			
355	360	365	
Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu			
370	375	380	
Leu Thr Pro Ala Ser Leu Pro Glu Ile Asp Gln Leu Asn Asp Asp Arg			
385	390	395	400
Asp His Thr Thr Val Leu Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala			
405	410	415	
Glu Ser Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu Ala			
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Cys Thr

<210> 106
<211> 1128
<212> DNA
<213> *Thermus thermophilus*

<400> 106

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<210> 107

<211> 376

<212> PRT

<213> *Thermus thermophilus*

<400> 107

Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
1 5 10 15

Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
20 25 30

Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn
35 40 45

Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu
50 55 60

Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser
65 70 75 80

Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln
85 90 95

Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser
100 105 110

Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu
115 120 125

Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu
130 135 140

Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr
145 150 155 160

Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe
165 170 175

Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro
180 185 190

Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
 195 200 205

 Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val
 210 215 220

 Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser
 225 230 235 240

 Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr
 245 250 255

 Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly
 260 265 270

 Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg
 275 280 285

 Gln Asn His Arg Val Asp Leu Leu Leu Glu Gly Arg Ile Leu Leu
 290 295 300

 Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
 305 310 315 320

 Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
 325 330 335

 Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
 340 345 350

 Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
 355 360 365

 Val Val Val Pro Leu Arg Val Glx
 370 375

<210> 108
 <211> 376
 <212> PRT
 <213> *Thermus thermophilus*

<400> 108
 Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
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 Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
 20 25 30

Leu	Gly	Leu	Tyr	Ala	Glu	Glu	Gly	Ala	Leu	Ile	Leu	Phe	Gly	Thr	Asn
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Gly	Glu	Val	Asp	Leu	Glu	Val	Arg	Leu	Pro	Ala	Glu	Ala	Gln	Ser	Leu
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Leu	Pro	Gly	Asp	Leu	Val	Ala	Leu	Gly	Leu	Ala	Ser	Glu	Pro	Gly	Gln
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Gly	Gly	Gln	Leu	Glu	Leu	Ser	Ser	Gly	Arg	Phe	Arg	Thr	Arg	Leu	Ser
									100			105		110	
Leu	Ala	Pro	Ala	Glu	Gly	Tyr	Pro	Glu	Leu	Leu	Val	Pro	Glu	Gly	Glu
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145									150			155		160	
Arg	Ala	Ile	Phe	Arg	Gly	Val	Gln	Leu	Glu	Phe	Ser	Pro	Gln	Gly	Phe
									165			170		175	
Arg	Ala	Val	Ala	Ser	Asp	Gly	Tyr	Arg	Leu	Ala	Leu	Tyr	Asp	Leu	Pro
									180			185		190	
Leu	Pro	Gln	Gly	Phe	Gln	Ala	Lys	Ala	Val	Val	Pro	Ala	Arg	Ser	Val
									195			200		205	
Asp	Glu	Met	Val	Arg	Val	Leu	Lys	Gly	Ala	Asp	Gly	Ala	Glu	Ala	Val
									210			215		220	
Leu	Ala	Leu	Gly	Glu	Gly	Val	Leu	Ala	Leu	Ala	Leu	Glu	Gly	Ser	
									225			230		235	240
Gly	Val	Arg	Met	Ala	Leu	Arg	Leu	Met	Glu	Gly	Glu	Phe	Pro	Asp	Tyr
									245			250		255	
Gln	Arg	Val	Ile	Pro	Gln	Glu	Phe	Ala	Leu	Lys	Val	Gln	Val	Glu	Gly
									260			265		270	
Glu	Ala	Leu	Arg	Glu	Ala	Val	Arg	Arg	Val	Ser	Val	Leu	Ser	Asp	Arg
									275			280		285	

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
290 295 300

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
305 310 315 320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
325 330 335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
340 345 350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
355 360 365

Val Val Val Pro Leu Arg Val Glx
370 375

<210> 109

<211> 367

<212> PRT

<213> Escherichia coli

<400> 109
Met Lys Phe Thr Val Glu Arg Glu His Leu Leu Lys Pro Leu Gln Gln
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Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
20 25 30

Leu Leu Leu Gln Val Ala Asp Gly Thr Leu Ser Leu Thr Gly Thr Asp
35 40 45

Leu Glu Met Glu Met Val Ala Arg Val Ala Leu Val Gln Pro His Glu
50 55 60

Pro Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Cys Arg
65 70 75 80

Gly Leu Pro Glu Gly Ala Glu Ile Ala Val Gln Leu Glu Gly Glu Arg
85 90 95

Met Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
100 105 110

Ala Ala Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe

115

120

125

Thr Leu Pro Gln Ala Thr Met Lys Arg Leu Ile Glu Ala Thr Gln Phe
 130 135 140

Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe
 145 150 155 160

Glu Thr Glu Gly Glu Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg
 165 170 175

Leu Ala Val Cys Ser Met Pro Ile Gly Gln Ser Leu Pro Ser His Ser
 180 185 190

Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Met Leu Asp
 195 200 205

Gly Gly Asp Asn Pro Leu Arg Val Gln Ile Gly Ser Asn Asn Ile Arg
 210 215 220

Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly Arg
 225 230 235 240

Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Asp Lys His Leu
 245 250 255

Glu Ala Gly Cys Asp Leu Leu Lys Gln Ala Phe Ala Arg Ala Ala Ile
 260 265 270

Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Leu Tyr Val Ser Glu Asn
 275 280 285

Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu Glu
 290 295 300

Ile Leu Asp Val Thr Tyr Ser Gly Ala Glu Met Glu Ile Gly Phe Asn
 305 310 315 320

Val Ser Tyr Val Leu Asp Val Leu Asn Ala Leu Lys Cys Glu Asn Val
 325 330 335

Arg Met Met Leu Thr Asp Ser Val Ser Ser Val Gln Ile Glu Asp Ala
 340 345 350

Ala Ser Gln Ser Ala Ala Tyr Val Val Met Pro Met Arg Leu Glx
 355 360 365

<210> 110
<211> 367
<212> PRT
<213> Proteus mirabilis

<400> 110
Met Lys Phe Ile Ile Glu Arg Glu Gln Leu Leu Lys Pro Leu Gln Gln
1 5 10 15
Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
20 25 30
Leu Leu Leu Lys Val Thr Glu Asn Thr Leu Ser Leu Thr Gly Thr Asp
35 40 45
Leu Glu Met Glu Met Met Ala Arg Val Ser Leu Ser Gln Ser His Glu
50 55 60
Ile Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Trp Arg
65 70 75 80
Gly Leu Pro Glu Gly Ala Glu Ile Ser Val Glu Leu Asp Gly Asp Arg
85 90 95
Leu Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
100 105 110
Ala Ser Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe
115 120 125
Thr Leu Pro Gln Ala Thr Leu Lys Arg Leu Ile Glu Ser Thr Gln Phe
130 135 140
Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe
145 150 155 160
Glu Thr Glu Asn Thr Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg
165 170 175
Leu Ala Val Cys Ala Met Asp Ile Gly Gln Ser Leu Pro Gly His Ser
180 185 190
Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Leu Leu Asp
195 200 205
Gly Ser Gly Glu Ser Leu Leu Gln Leu Gln Ile Gly Ser Asn Asn Leu
210 215 220

Arg Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly
225 230 235 240

Arg Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Thr Lys Thr
245 250 255

Val Ile Ala Gly Cys Asp Ile Leu Lys Gln Ala Phe Ser Arg Ala Ala
260 265 270

Ile Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Ile Asn Leu Thr Asn
275 280 285

Gly Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu
290 295 300

Glu Ile Val Asp Val Gln Tyr Gln Gly Glu Glu Met Glu Ile Gly Phe
305 310 315 320

Asn Val Ser Tyr Leu Leu Asp Val Leu Asn Thr Leu Lys Cys Glu Glu
325 330 335

Val Lys Leu Leu Leu Thr Asp Ala Val Ser Ser Val Gln Val Glu Asn
340 345 350

Val Ala Ser Ala Ala Ala Ala Tyr Val Val Met Pro Met Arg Leu
355 360 365

<210> 111

<211> 366

<212> PRT

<213> Haemophilus influenzae

<400> 111

Met Gln Phe Ser Ile Ser Arg Glu Asn Leu Leu Lys Pro Leu Gln Gln
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Val Cys Gly Val Leu Ser Asn Arg Pro Asn Ile Pro Val Leu Asn Asn
20 25 30

Val Leu Leu Gln Ile Glu Asp Tyr Arg Leu Thr Ile Thr Gly Thr Asp
35 40 45

Leu Glu Val Glu Leu Ser Ser Gln Thr Gln Leu Ser Ser Ser Glu
50 55 60

Asn Gly Thr Phe Thr Ile Pro Ala Lys Lys Phe Leu Asp Ile Cys Arg
65 70 75 80

Thr Leu Ser Asp Asp Ser Glu Ile Thr Val Thr Phe Glu Gln Asp Arg
85 90 95

Ala Leu Val Gln Ser Gly Arg Ser Arg Phe Thr Leu Ala Thr Gln Pro
100 105 110

Ala Glu Glu Tyr Pro Asn Leu Thr Asp Trp Gln Ser Glu Val Asp Phe
115 120 125

Glu Leu Pro Gln Asn Thr Leu Arg Arg Leu Ile Glu Ala Thr Gln Phe
130 135 140

Ser Met Ala Asn Gln Asp Ala Arg Tyr Phe Leu Asn Gly Met Lys Phe
145 150 155 160

Glu Thr Glu Gly Asn Leu Leu Arg Thr Val Ala Thr Asp Gly His Arg
165 170 175

Leu Ala Val Cys Thr Ile Ser Leu Glu Gln Glu Leu Gln Asn His Ser
180 185 190

Val Ile Leu Pro Arg Lys Gly Val Leu Glu Leu Val Arg Leu Leu Glu
195 200 205

Thr Asn Asp Glu Pro Ala Arg Leu Gln Ile Gly Thr Asn Asn Leu Arg
210 215 220

Val His Leu Lys Asn Thr Val Phe Thr Ser Lys Leu Ile Asp Gly Arg
225 230 235 240

Phe Pro Asp Tyr Arg Arg Val Leu Pro Arg Asn Ala Thr Lys Ile Val
245 250 255

Glu Gly Asn Trp Glu Met Leu Lys Gln Ala Phe Ala Arg Ala Ser Ile
260 265 270

Leu Ser Asn Glu Arg Ala Arg Ser Val Arg Leu Ser Leu Lys Glu Asn
275 280 285

Gln Leu Lys Ile Thr Ala Ser Asn Thr Glu His Glu Glu Ala Glu Glu
290 295 300

Ile Val Asp Val Asn Tyr Asn Gly Glu Glu Leu Glu Val Gly Phe Asn
305 310 315 320

Val Thr Tyr Ile Leu Asp Val Leu Asn Ala Leu Lys Cys Asn Gln Val
325 330 335

Arg Met Cys Leu Thr Asp Ala Phe Ser Ser Cys Leu Ile Glu Asn Cys
 340 345 350
 Glu Asp Ser Ser Cys Glu Tyr Val Ile Met Pro Met Arg Leu
 355 360 365

 <210> 112
 <211> 367
 <212> PRT
 <213> Pseudomonas putida

 <400> 112
 Met His Phe Thr Ile Gln Arg Glu Ala Leu Leu Lys Pro Leu Gln Leu
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 Val Ala Gly Val Val Glu Arg Arg Gln Thr Leu Pro Val Leu Ser Asn
 20 25 30
 Val Leu Leu Val Val Gln Gly Gln Gln Leu Ser Leu Thr Gly Thr Asp
 35 40 45
 Leu Glu Val Glu Leu Val Gly Arg Val Gln Leu Glu Glu Pro Ala Glu
 50 55 60
 Pro Gly Glu Ile Thr Val Pro Ala Arg Lys Leu Met Asp Ile Cys Lys
 65 70 75 80
 Ser Leu Pro Asn Asp Ala Leu Ile Asp Ile Lys Val Asp Glu Gln Lys
 85 90 95
 Leu Leu Val Lys Ala Gly Arg Ser Arg Phe Thr Leu Ser Thr Leu Pro
 100 105 110
 Ala Asn Asp Phe Pro Thr Val Glu Glu Gly Pro Gly Ser Leu Thr Cys
 115 120 125
 Asn Leu Glu Gln Ser Lys Leu Arg Arg Leu Ile Glu Arg Thr Ser Phe
 130 135 140
 Ala Met Ala Gln Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu
 145 150 155 160
 Glu Val Ser Arg Asn Thr Leu Arg Ala Val Ser Thr Asp Gly His Arg
 165 170 175
 Leu Ala Leu Cys Ser Met Ser Ala Pro Ile Glu Gln Glu Asp Arg His

180	185	190
Gln Val Ile Val Pro Arg Lys Gly Ile Leu Glu Leu Ala Arg Leu Leu		
195	200	205
Thr Asp Pro Glu Gly Met Val Ser Ile Val Leu Gly Gln His His Ile		
210	215	220
Arg Ala Thr Thr Gly Glu Phe Thr Phe Thr Ser Lys Leu Val Asp Gly		
225	230	235
Lys Phe Pro Asp Tyr Glu Arg Val Leu Pro Lys Gly Gly Asp Lys Leu		
245	250	255
Val Val Gly Asp Arg Gln Ala Leu Arg Glu Ala Phe Ser Arg Thr Ala		
260	265	270
Ile Leu Ser Asn Glu Lys Tyr Arg Gly Ile Arg Leu Gln Leu Ala Ala		
275	280	285
Gly Gln Leu Lys Ile Gln Ala Asn Asn Pro Glu Gln Glu Ala Glu		
290	295	300
Glu Glu Ile Ser Val Asp Tyr Glu Gly Ser Ser Leu Glu Ile Gly Phe		
305	310	315
Asn Val Ser Tyr Leu Leu Asp Val Leu Gly Val Met Thr Thr Glu Gln		
325	330	335
Val Arg Leu Ile Leu Ser Asp Ser Asn Ser Ser Ala Leu Leu Gln Glu		
340	345	350
Ala Gly Asn Asp Asp Ser Ser Tyr Val Val Met Pro Met Arg Leu		
355	360	365
<210> 113		
<211> 366		
<212> PRT		
<213> Buchnera aphidicola		
<400> 113		
Met Lys Phe Thr Ile Gln Asn Asp Ile Leu Thr Lys Asn Leu Lys Lys		
1	5	10
Ile Thr Arg Val Leu Val Lys Asn Ile Ser Phe Pro Ile Leu Glu Asn		
20	25	30

Ile Leu Ile Gln Val Glu Asp Gly Thr Leu Ser Leu Thr Thr Thr Asn
 35 40 45

Leu Glu Ile Glu Leu Ile Ser Lys Ile Glu Ile Ile Thr Lys Tyr Ile
 50 55 60

Pro Gly Lys Thr Thr Ile Ser Gly Arg Lys Ile Leu Asn Ile Cys Arg
 65 70 75 80

Thr Leu Ser Glu Lys Ser Lys Ile Lys Met Gln Leu Lys Asn Lys Lys
 85 90 95

Met Tyr Ile Ser Ser Glu Asn Ser Asn Tyr Ile Leu Ser Thr Leu Ser
 100 105 110

Ala Asp Thr Phe Pro Asn His Gln Asn Phe Asp Tyr Ile Ser Lys Phe
 115 120 125

Asp Ile Ser Ser Asn Ile Leu Lys Glu Met Ile Glu Lys Thr Glu Phe
 130 135 140

Ser Met Gly Lys Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu
 145 150 155 160

Glu Lys Lys Asp Lys Phe Leu Arg Ser Val Ala Thr Asp Gly Tyr Arg
 165 170 175

Leu Ala Ile Ser Tyr Thr Gln Leu Lys Lys Asp Ile Asn Phe Phe Ser
 180 185 190

Ile Ile Ile Pro Asn Lys Ala Val Met Glu Leu Leu Lys Leu Leu Asn
 195 200 205

Thr Gln Pro Gln Leu Leu Asn Ile Leu Ile Gly Ser Asn Ser Ile Arg
 210 215 220

Ile Tyr Thr Lys Asn Leu Ile Phe Thr Thr Gln Leu Ile Glu Gly Glu
 225 230 235 240

Tyr Pro Asp Tyr Lys Ser Val Leu Phe Lys Glu Lys Lys Asn Pro Ile
 245 250 255

Ile Thr Asn Ser Ile Leu Leu Lys Lys Ser Leu Leu Arg Val Ala Ile
 260 265 270

Leu Ala His Glu Lys Phe Cys Gly Ile Glu Ile Lys Ile Glu Asn Gly
 275 280 285

Lys Phe Lys Val Leu Ser Asp Asn Gln Glu Glu Glu Thr Ala Glu Asp
290 295 300
Leu Phe Glu Ile Asp Tyr Phe Gly Glu Lys Ile Glu Ile Ser Ile Asn
305 310 315 320
Val Tyr Tyr Leu Leu Asp Val Ile Asn Asn Ile Lys Ser Glu Asn Ile
325 330 335
Ala Leu Phe Leu Asn Lys Ser Ser Ile Gln Ile Glu Ala Glu
340 345 350
Asn Asn Ser Ser Asn Ala Tyr Val Val Met Leu Leu Lys Arg
355 360 365

<210> 114
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 114 39
gtgtggatcc tcgtccccct catgcgcgac caggaaggg

<210> 115
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 115 27
gtgtggatcc gtggtgacct tagccac

<210> 116
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 116

ttcgtgtccg aggaccttgt ggtccacaac

30

<210> 117

<211> 3514

<212> DNA

<213> Aquifex aeolicus

<400> 117

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tcgcaaagga gatgaggaat acccttata tattcttaaa aagagagcaa gcccctaaacg 3300
gcgttgcgcga aaaactaaag ggaatttattt aaaaacaacag gacggaggac ggatacaact 3360
tggttctcac gtttgcactt gtagactact tcgttgattt agcactccca caagatatga 3420
aactaaaggc tgacagaaag gttttagagg agatagaaaa actggagtg aaggtcataa 3480
tttagtaat aacccttact tccgagtagt cccc 3514

<210> 118
<211> 1161
<212> PRT
<213> Aquifex aeolicus

<400> 118
Met Ser Lys Asp Phe Val His Leu His Leu His Thr Gln Phe Ser Leu
1 5 10 15

Leu Asp Gly Ala Ile Lys Ile Asp Glu Leu Val Lys Lys Ala Lys Glu
20 25 30

Tyr Gly Tyr Lys Ala Val Gly Met Ser Asp His Gly Asn Leu Phe Gly
35 40 45

Ser Tyr Lys Phe Tyr Lys Ala Leu Lys Ala Glu Gly Ile Lys Pro Ile
50 55 60

Ile Gly Met Glu Ala Tyr Phe Thr Thr Gly Ser Arg Phe Asp Arg Lys
65 70 75 80

Thr Lys Thr Ser Glu Asp Asn Ile Thr Asp Lys Tyr Asn His His Leu
85 90 95

Ile Leu Ile Ala Lys Asp Asp Lys Gly Leu Lys Asn Leu Met Lys Leu

100	105	110
Ser Thr Leu Ala Tyr Lys Glu Gly Phe Tyr Tyr Lys Pro Arg Ile Asp		
115	120	125
Tyr Glu Leu Leu Glu Lys Tyr Gly Glu Gly Leu Ile Ala Leu Thr Ala		
130	135	140
Cys Leu Lys Gly Val Pro Thr Tyr Tyr Ala Ser Ile Asn Glu Val Lys		
145	150	155
Lys Ala Glu Glu Trp Val Lys Lys Phe Lys Asp Ile Phe Gly Asp Asp		
165	170	175
Leu Tyr Leu Glu Leu Gln Ala Asn Asn Ile Pro Glu Gln Glu Val Ala		
180	185	190
Asn Arg Asn Leu Ile Glu Ile Ala Lys Lys Tyr Asp Val Lys Leu Ile		
195	200	205
Ala Thr Gln Asp Ala His Tyr Leu Asn Pro Glu Asp Arg Tyr Ala His		
210	215	220
Thr Val Leu Met Ala Leu Gln Met Lys Lys Thr Ile His Glu Leu Ser		
225	230	240
Ser Gly Asn Phe Lys Cys Ser Asn Glu Asp Leu His Phe Ala Pro Pro		
245	250	255
Glu Tyr Met Trp Lys Lys Phe Glu Gly Lys Phe Glu Gly Trp Glu Lys		
260	265	270
Ala Leu Leu Asn Thr Leu Glu Val Met Glu Lys Thr Ala Asp Ser Phe		
275	280	285
Glu Ile Phe Glu Asn Ser Thr Tyr Leu Leu Pro Lys Tyr Asp Val Pro		
290	295	300
Pro Asp Lys Thr Leu Glu Glu Tyr Leu Arg Glu Leu Ala Tyr Lys Gly		
305	310	315
Leu Arg Gln Arg Ile Glu Arg Gly Gln Ala Lys Asp Thr Lys Glu Tyr		
325	330	335
Trp Glu Arg Leu Glu Tyr Glu Leu Glu Val Ile Asn Lys Met Gly Phe		
340	345	350
Ala Gly Tyr Phe Leu Ile Val Gln Asp Phe Ile Asn Trp Ala Lys Lys		

355	360	365
Asn Asp Ile Pro Val Gly Pro Gly Arg Gly Ser Ala Gly Gly Ser Leu		
370	375	380
Val Ala Tyr Ala Ile Gly Ile Thr Asp Val Asp Pro Ile Lys His Gly		
385	390	395
Phe Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp		
405	410	415
Ile Asp Val Asp Phe Cys Gln Asp Asn Arg Glu Lys Val Ile Glu Tyr		
420	425	430
Val Arg Asn Lys Tyr Gly His Asp Asn Val Ala Gln Ile Ile Thr Tyr		
435	440	445
Asn Val Met Lys Ala Lys Gln Thr Leu Arg Asp Val Ala Arg Ala Met		
450	455	460
Gly Leu Pro Tyr Ser Thr Ala Asp Lys Leu Ala Lys Leu Ile Pro Gln		
465	470	475
Gly Asp Val Gln Gly Thr Trp Leu Ser Leu Glu Glu Met Tyr Lys Thr		
485	490	495
Pro Val Glu Glu Leu Leu Gln Lys Tyr Gly Glu His Arg Thr Asp Ile		
500	505	510
Glu Asp Asn Val Lys Lys Phe Arg Gln Ile Cys Glu Glu Ser Pro Glu		
515	520	525
Ile Lys Gln Leu Val Glu Thr Ala Leu Lys Leu Glu Gly Leu Thr Arg		
530	535	540
His Thr Ser Leu His Ala Ala Gly Val Val Ile Ala Pro Lys Pro Leu		
545	550	555
Ser Glu Leu Val Pro Leu Tyr Tyr Asp Lys Glu Gly Glu Val Ala Thr		
565	570	575
Gln Tyr Asp Met Val Gln Leu Glu Glu Leu Gly Leu Leu Lys Met Asp		
580	585	590
Phe Leu Gly Leu Lys Thr Leu Thr Glu Leu Lys Leu Met Lys Glu Leu		
595	600	605
Ile Lys Glu Arg His Gly Val Asp Ile Asn Phe Leu Glu Leu Pro Leu		

610	615	620
Asp Asp Pro Lys Val Tyr Lys Leu Leu Gln Glu Gly Lys Thr Thr Gly		
625	630	635
640		
Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu Leu Leu Lys Lys Leu		
645	650	655
660		
Lys Pro Asp Ser Phe Asp Asp Ile Val Ala Val Leu Ala Leu Tyr Arg		
665	670	
675		
Pro Gly Pro Leu Lys Ser Gly Leu Val Asp Thr Tyr Ile Lys Arg Lys		
680	685	
690		
His Gly Lys Glu Pro Val Glu Tyr Pro Phe Pro Glu Leu Glu Pro Val		
695	700	
705		
Leu Lys Glu Thr Tyr Gly Val Ile Val Tyr Gln Glu Gln Val Met Lys		
710	715	720
725		
Met Ser Gln Ile Leu Ser Gly Phe Thr Pro Gly Glu Ala Asp Thr Leu		
730	735	
740		
Arg Lys Ala Ile Gly Lys Lys Ala Asp Leu Met Ala Gln Met Lys		
745	750	
755		
Asp Lys Phe Ile Gln Gly Ala Val Glu Arg Gly Tyr Pro Glu Glu Lys		
760	765	
770		
Ile Arg Lys Leu Trp Glu Asp Ile Glu Lys Phe Ala Ser Tyr Ser Phe		
775	780	
785		
Asn Lys Ser His Ser Val Ala Tyr Gly Tyr Ile Ser Tyr Trp Thr Ala		
790	795	800
805		
Tyr Val Lys Ala His Tyr Pro Ala Glu Phe Phe Ala Val Lys Leu Thr		
810	815	
820		
Thr Glu Lys Asn Asp Asn Lys Phe Leu Asn Leu Ile Lys Asp Ala Lys		
825	830	
835		
Leu Phe Gly Phe Glu Ile Leu Pro Pro Asp Ile Asn Lys Ser Asp Val		
840	845	
850		
Gly Phe Thr Ile Glu Gly Glu Asn Arg Ile Arg Phe Gly Leu Ala Arg		
855	860	
865		
Ile Lys Gly Val Gly Glu Glu Thr Ala Lys Ile Ile Val Glu Ala Arg		

865	870	875	880
Lys Lys Tyr Lys Gln Phe Lys Gly Leu Ala Asp Phe Ile Asn Lys Thr			
885		890	895
Lys Asn Arg Lys Ile Asn Lys Lys Val Val Glu Ala Leu Val Lys Ala			
900	905		910
Gly Ala Phe Asp Phe Thr Lys Lys Arg Lys Glu Leu Leu Ala Lys			
915	920	925	
Val Ala Asn Ser Glu Lys Ala Leu Met Ala Thr Gln Asn Ser Leu Phe			
930	935	940	
Gly Ala Pro Lys Glu Glu Val Glu Glu Leu Asp Pro Leu Lys Leu Glu			
945	950	955	960
Lys Glu Val Leu Gly Phe Tyr Ile Ser Gly His Pro Leu Asp Asn Tyr			
965	970	975	
Glu Lys Leu Leu Lys Asn Arg Tyr Thr Pro Ile Glu Asp Leu Glu Glu			
980	985	990	
Trp Asp Lys Glu Ser Glu Ala Val Leu Thr Gly Val Ile Thr Glu Leu			
995	1000	1005	
Lys Val Lys Lys Thr Lys Asn Gly Asp Tyr Met Ala Val Phe Asn Leu			
1010	1015	1020	
Val Asp Lys Thr Gly Leu Ile Glu Cys Val Val Phe Pro Gly Val Tyr			
1025	1030	1035	1040
Glu Glu Ala Lys Glu Leu Ile Glu Glu Asp Arg Val Val Val Lys			
1045	1050	1055	
Gly Phe Leu Asp Glu Asp Leu Glu Thr Glu Asn Val Lys Phe Val Val			
1060	1065	1070	
Lys Glu Val Phe Ser Pro Glu Glu Phe Ala Lys Glu Met Arg Asn Thr			
1075	1080	1085	
Leu Tyr Ile Phe Leu Lys Arg Glu Gln Ala Leu Asn Gly Val Ala Glu			
1090	1095	1100	
Lys Leu Lys Gly Ile Ile Glu Asn Asn Arg Thr Glu Asp Gly Tyr Asn			
1105	1110	1115	1120
Leu Val Leu Thr Val Asp Leu Gly Asp Tyr Phe Val Asp Leu Ala Leu			

1125

1130

1135

Pro Gln Asp Met Lys Leu Lys Ala Asp Arg Lys Val Val Glu Glu Ile
1140 1145 1150

Glu Lys Leu Gly Val Lys Val Ile Ile
1155 1160

<210> 119

<211> 2408

<212> DNA

<213> Aquifex aeolicus

<400> 119

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cagaagctc ccgtaaaggat actcaaaaac gctataaaaa acgacagagt ggctcacgcc 120
tacccctttg ccggaccgag ggggggttggg aagacgacta ttgcaagaat tctcgcaaaa 180
gcttgaact gtaaaaatcc ctccaaaggt gagccctgcg gtgagtgca aaactgcagg 240
gagatagaca ggggtgtgtt ccctgactta attgaaatgg atgcccgcctc aaacaggggt 300
atagacgacg taagggcatt aaaagaagcg gtcaattaca aacctataaa aggaaagtac 360
aaggtttaca taatagacga agtcacatg ctcacgaaag aagcttcaa cgctcttta 420
aaaaccctcg aagagcccccc tcccagaact gtttctgtcc tttgtaccac ggagtacgac 480
aaaattcttc ccacgatact ctcaaggtgt cagaggataa tcttctcaaa ggttaagaaag 540
gaaaaagtaa tagagtatct aaaaaagata tgtgaaaagg aagggtttaga gtgcgaagag 600
ggagcccttg aggttctggc tcatgcctct gaagggtgca tgagggatgc agcctctctc 660
ctggaccagg cgagcgttta cggggaaaggc agggtaacaa aagaagtagt ggagaacttc 720
ctcggattc tcagtcagga aagcgtttagg agtttctga aattgcttct gaactcagaa 780
gtggacgaag ctataaagtt ctcagagaaa ctctcagaaa agggctacaa cctgaccaag 840
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cccgaaagcg tggtcagaa ctggcaggat tacgaagact tcaaagacta ccctctggaa 960
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gtatcccagc tcggaagtgt ggttaaggaa accaaaaagg aagaaaaagaa agttaagat 1140
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aagaatttg actcactaaa ggagacttt ctttttttag agtttgaacc cgtggaggat 1380
aaaaaaaaac ctcagaagtc cagcgggacg aggctgttt aaaggttaag gagctttca 1440
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tttgtctctt actacgacta ttaccaacct gaagcctaca ttcccgaaaa agatttatac 2040
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ccgttctaga aaggaggac gttatagtag ttgcttcgt ttcttgata tacggactcg 2160
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tgagtaagct cctgaggaaa ctcgttgac taggatatca gagaaatgac tttgccataa 2280
agagggctac cttctcggtt agggagacg tggtagat agtcccttct cacacggaaag 2340
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ctctgaac 2408

<210> 120
<211> 473
<212> PRT
<213> Aquifex aeolicus

<400> 120
Met Asn Tyr Val Pro Phe Ala Arg Lys Tyr Arg Pro Lys Phe Phe Arg
1 5 10 15

Glu Val Ile Gly Gln Glu Ala Pro Val Arg Ile Leu Lys Asn Ala Ile
20 25 30

Lys Asn Asp Arg Val Ala His Ala Tyr Leu Phe Ala Gly Pro Arg Gly
35 40 45

Val Gly Lys Thr Thr Ile Ala Arg Ile Leu Ala Lys Ala Leu Asn Cys
50 55 60

Lys Asn Pro Ser Lys Gly Glu Pro Cys Gly Glu Cys Glu Asn Cys Arg
65 70 75 80

Glu Ile Asp Arg Gly Val Phe Pro Asp Leu Ile Glu Met Asp Ala Ala
85 90 95

Ser Asn Arg Gly Ile Asp Asp Val Arg Ala Leu Lys Glu Ala Val Asn
100 105 110

Tyr Lys Pro Ile Lys Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Ala
115 120 125

His Met Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Pro Arg Thr Val Phe Val Leu Cys Thr Thr Glu Tyr Asp
145 150 155 160

Lys Ile Leu Pro Thr Ile Leu Ser Arg Cys Gln Arg Ile Ile Phe Ser
165 170 175

Lys Val Arg Lys Glu Lys Val Ile Glu Tyr Leu Lys Lys Ile Cys Glu
180 185 190

Lys Glu Gly Ile Glu Cys Glu Glu Gly Ala Leu Glu Val Leu Ala His
195 200 205

Ala Ser Glu Gly Cys Met Arg Asp Ala Ala Ser Leu Leu Asp Gln Ala
210 215 220

Ser Val Tyr Gly Glu Gly Arg Val Thr Lys Glu Val Val Glu Asn Phe
225 230 235 240

Leu Gly Ile Leu Ser Gln Glu Ser Val Arg Ser Phe Leu Lys Leu Leu
245 250 255

Leu Asn Ser Glu Val Asp Glu Ala Ile Lys Phe Leu Arg Glu Leu Ser
260 265 270

Glu Lys Gly Tyr Asn Leu Thr Lys Phe Trp Glu Met Leu Glu Glu Glu
275 280 285

Val Arg Asn Ala Ile Leu Val Lys Ser Leu Lys Asn Pro Glu Ser Val
290 295 300

Val Gln Asn Trp Gln Asp Tyr Glu Asp Phe Lys Asp Tyr Pro Leu Glu
305 310 315 320

Ala Leu Leu Tyr Val Glu Asn Leu Ile Asn Arg Gly Lys Val Glu Ala
325 330 335

Arg Thr Arg Glu Pro Leu Arg Ala Phe Glu Leu Ala Val Ile Lys Ser
340 345 350

Leu Ile Val Lys Asp Ile Ile Pro Val Ser Gln Leu Gly Ser Val Val
355 360 365

Lys Glu Thr Lys Lys Glu Glu Lys Lys Val Glu Val Lys Glu Glu Pro
370 375 380

Lys Val Lys Glu Glu Lys Pro Lys Glu Gln Glu Glu Asp Arg Phe Gln
385 390 395 400

Lys Val Leu Asn Ala Val Asp Gly Lys Ile Leu Lys Arg Ile Leu Glu
405 410 415

Gly Ala Lys Arg Glu Glu Arg Asp Gly Lys Ile Val Leu Lys Ile Glu
420 425 430

Ala Ser Tyr Leu Arg Thr Met Lys Lys Glu Phe Asp Ser Leu Lys Glu
435 440 445

Thr Phe Pro Phe Leu Glu Phe Glu Pro Val Glu Asp Lys Lys Pro
450 455 460

Gln Lys Ser Ser Gly Thr Arg Leu Phe
465 470

<210> 121

<211> 1090

<212> DNA

<213> Aquifex aeolicus

<400> 121

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acggaaaaaa aagccgcact cccgatactc gcgaacttct tactctccgc aaaagaggaa 120
aacttaatcg taagggcaac ggacttggaa aactaccttgc tagtctccgt aaagggggag 180
gttgaagagg aaggagaggt ttgcgtccac tctcaaaaac tctacgatat agtcaagaac 240
ttaaattccg cttacgttta ctttcatacgt gaaggtgaaa aactcgtcat aacgggagga 300
aagagtacgt acaaacttcc gacagctccc gcggaggact ttcccgaatt tccagaaatc 360
gtagaaggag gagaaacact ttcggaaac cttctcggtt acggaataga aaaggttagag 420
tacgccatag cgaaggaaaga agcgaacata gcccattcagg gaatgtatct gagaggatac 480
gaggacagaa ttcactttgt gttcggacgg tcacaggctt gcactttatg aacctctacg 540
taaacattga aaagagtgaa gacgagtctt ttgcttactt ctccactccc gagtgaaac 600
tcgcccgttag ctccctggaag gagaattccc ggactacatg agtgcatacc ctgaggagtt 660
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tgagttcgcg gatccggagt tcggagaagc gagagaggaa attgaagtgg agtacacggg 840
agagcccttt gagataggat tcaacggaaa tacttatgg aggcgcttga cgcctacgac 900
agcgaaagag tgtggttcaa gttcacaacc cccgacacgg ccactttatt ggaggctgaa 960
gattacgaaa aggaaccttta caagtgcata ataatgccga tgagggtgta gccataaaa 1020
aagcttaat cttttatttgc agcttgcgttcc tttaattcc tgcgttttagc gaagccaaac 1080
ccaagtcttc 1090

<210> 122

<211> 363

<212> PRT

<213> Aquifex aeolicus

<400> 122

Met Arg Val Lys Val Asp Arg Glu Glu Leu Glu Glu Val Leu Lys Lys
1 5 10 15

Ala Arg Glu Ser Thr Glu Lys Lys Ala Ala Leu Pro Ile Leu Ala Asn

20

25

30

Phe Leu Leu Ser Ala Lys Glu Glu Asn Leu Ile Val Arg Ala Thr Asp
 35 40 45

Leu Glu Asn Tyr Leu Val Val Ser Val Lys Gly Glu Val Glu Glu Glu
 50 55 60

Gly Glu Val Cys Val His Ser Gln Lys Leu Tyr Asp Ile Val Lys Asn
 65 70 75 80

Leu Asn Ser Ala Tyr Val Tyr Leu His Thr Glu Gly Glu Lys Leu Val
 85 90 95

Ile Thr Gly Gly Lys Ser Thr Tyr Lys Leu Pro Thr Ala Pro Ala Glu
 100 105 110

Asp Phe Pro Glu Phe Pro Glu Ile Val Glu Gly Gly Glu Thr Leu Ser
 115 120 125

Gly Asn Leu Leu Val Asn Gly Ile Glu Lys Val Glu Tyr Ala Ile Ala
 130 135 140

Lys Glu Glu Ala Asn Ile Ala Leu Gln Gly Met Tyr Leu Arg Gly Tyr
 145 150 155 160

Glu Asp Arg Ile His Phe Val Gly Ser Asp Gly His Arg Leu Ala Leu
 165 170 175

Tyr Glu Pro Leu Gly Glu Phe Ser Lys Glu Leu Leu Ile Pro Arg Lys
 180 185 190

Ser Leu Lys Val Leu Lys Lys Leu Ile Thr Gly Ile Glu Asp Val Asn
 195 200 205

Ile Glu Lys Ser Glu Asp Glu Ser Phe Ala Tyr Phe Ser Thr Pro Glu
 210 215 220

Trp Lys Leu Ala Val Arg Leu Leu Glu Gly Glu Phe Pro Asp Tyr Met
 225 230 235 240

Ser Val Ile Pro Glu Glu Phe Ser Ala Glu Val Leu Phe Glu Thr Glu
 245 250 255

Glu Val Leu Lys Val Leu Lys Arg Leu Lys Ala Leu Ser Glu Gly Lys
 260 265 270

Val Phe Pro Val Lys Ile Thr Leu Ser Glu Asn Leu Ala Ile Phe Glu

275

280

285

Phe Ala Asp Pro Glu Phe Gly Glu Ala Arg Glu Glu Ile Glu Val Glu
290 295 300

Tyr Thr Gly Glu Pro Phe Glu Ile Gly Phe Asn Gly Lys Tyr Leu Met
305 310 315 320

Glu Ala Leu Asp Ala Tyr Asp Ser Glu Arg Val Trp Phe Lys Phe Thr
325 330 335

Thr Pro Asp Thr Ala Thr Leu Leu Glu Ala Glu Asp Tyr Glu Lys Glu
340 345 350

Pro Tyr Lys Cys Ile Ile Met Pro Met Arg Val
355 360

<210> 123

<211> 1093

<212> DNA

<213> Aquifex aeolicus

<400> 123

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gaaaagtacg gggagaatta cacggttctg tggggggatg agataagcga ggaggaattc 180
tacactgccc tttccgagac cagtatattc ggccgttcaa aggaaaaagc ggtggtcatt 240
tacaacttcg gggatttcct gaagaagctc ggaaggaaga aaaaggaaaa agaaaggctt 300
ataaaaagtcc tcagaaacgt aaagagtaac tacgtattta tagtgtacga tgcgaaactc 360
cagaaacagg aactttctc ggaacctctg aaatccgtag cgtcttcgg cggatatagt 420
gtagcaaaca ggctgagcaa ggagaggata aaacagctc tccttaagaa gttcaaagaa 480
aaagggataa acgtagaaaa cgtgccctt gaataccctc tccagctcac gggttacaac 540
ttgatggagc tcaaacttga ggttggaaaa ctgatagatt acgcaagtga aaagaaaatt 600
ttaacactcg atgaggtaaa gagagtagcc ttctcagtc cagaaaacgt aaacgtattt 660
gagttcggtt atttactcct cttaaaagat tacggaaaagg ctcttaaagt tttggactcc 720
ctcatttcct tcggaataca cccctccag attatgaaaa tcctgtcctc ctatgtctta 780
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agcgtgggaa taaagaacaa ctttctcaag atgaagttca aatcttactt aaaggcaaac 900
tctaaagagg acttgaagaa cctaattcctc tccctccaga ggatagacgc tttttctaaa 960
ctttactttc aggacacagt gcagttgctg gggatttctt gacctaaga ctggagaggg 1020
aagttgtgaa aaataacttct catggtgat aatcttttt atgaagtttgcgt 1080
ttttcccggt tct 1093

<210> 124

<211> 350

<212> PRT

<213> Aquifex aeolicus

<400> 124

Val Glu Thr Thr Ile Phe Gln Phe Gln Lys Thr Phe Phe Thr Lys Pro
1 5 10 15

Pro Lys Glu Arg Val Phe Val Leu His Gly Glu Glu Gln Tyr Leu Ile
20 25 30

Arg Thr Phe Leu Ser Lys Leu Lys Glu Lys Tyr Gly Glu Asn Tyr Thr
35 40 45

Val Leu Trp Gly Asp Glu Ile Ser Glu Glu Glu Phe Tyr Thr Ala Leu
50 55 60

Ser Glu Thr Ser Ile Phe Gly Gly Ser Lys Glu Lys Ala Val Val Ile
65 70 75 80

Tyr Asn Phe Gly Asp Phe Leu Lys Lys Leu Gly Arg Lys Lys Lys Glu
85 90 95

Lys Glu Arg Leu Ile Lys Val Leu Arg Asn Val Lys Ser Asn Tyr Val
100 105 110

Phe Ile Val Tyr Asp Ala Lys Leu Gln Lys Gln Glu Leu Ser Ser Glu
115 120 125

Pro Leu Lys Ser Val Ala Ser Phe Gly Gly Ile Val Val Ala Asn Arg
130 135 140

Leu Ser Lys Glu Arg Ile Lys Gln Leu Val Leu Lys Lys Phe Lys Glu
145 150 155 160

Lys Gly Ile Asn Val Glu Asn Asp Ala Leu Glu Tyr Leu Leu Gln Leu
165 170 175

Thr Gly Tyr Asn Leu Met Glu Leu Lys Leu Glu Val Glu Lys Leu Ile
180 185 190

Asp Tyr Ala Ser Glu Lys Lys Ile Leu Thr Leu Asp Glu Val Lys Arg
195 200 205

Val Ala Phe Ser Val Ser Glu Asn Val Asn Val Phe Glu Phe Val Asp
210 215 220

Leu Leu Leu Lys Asp Tyr Glu Lys Ala Leu Lys Val Leu Asp Ser
225 230 235 240

Leu Ile Ser Phe Gly Ile His Pro Leu Gln Ile Met Lys Ile Leu Ser
 245 250 255
 Ser Tyr Ala Leu Lys Leu Tyr Thr Leu Lys Arg Leu Glu Glu Lys Gly
 260 265 270
 Glu Asp Leu Asn Lys Ala Met Glu Ser Val Gly Ile Lys Asn Asn Phe
 275 280 285
 Leu Lys Met Lys Phe Lys Ser Tyr Leu Lys Ala Asn Ser Lys Glu Asp
 290 295 300
 Leu Lys Asn Leu Ile Leu Ser Leu Gln Arg Ile Asp Ala Phe Ser Lys
 305 310 315 320
 Leu Tyr Phe Gln Asp Thr Val Gln Leu Leu Arg Asp Phe Leu Thr Ser
 325 330 335
 Arg Leu Glu Arg Glu Val Val Lys Asn Thr Ser His Gly Gly
 340 345 350

<210> 125
 <211> 1051
 <212> DNA
 <213> Aquifex aeolicus

<400> 125
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 ttatgttaagg aaaacgtacc tggggatgctt gaagttgtcc ctccgtcaaa cacgtaaacg 180
 agctggagga agccttctt aaaggagaaa tagaagactt taaagtttat aagacaagga 240
 cggtaaaaag cacttcgttt accttatgg cgaacatccc gactttgtgg taataatccc 300
 gagcggacat tacataaaga tagaacagat aaggaagtt aagaactttg cctatgtgaa 360
 gcccgcacta agcaggagaa aagtaattat aatagacgac gcccacgcga tgacctctca 420
 ggcggcaaac gctctttaa aggtatttggaa agagccaccc gcggacacca cctttatctt 480
 gaccacgaac aggcgttctg caatcctgcc gactatcctc tccagaacctt ttcaagtggaa 540
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 gaaaactcttctt ggaggcagtc taaaaaggcc tatcttacta aaggaaaaca aagatatcc 660
 aaacaaaatgtt aaggaattct tggaaaacgcg gccgttaaaa gtttacaagc ttcaagtggaa 720
 attcgaaaag tgggaacctg aaaagcaaaa actcttcctt gaaattatgg aagaatttgg 780
 atctcaaaaa ttgaccgaag agaaaaaaga caattacacc taccttctt atacgatcag 840
 actctttaaa gacggactcg caaggggtgt aaacgaacct ctgtggctgt ttacgttagc 900
 cgttcaggcg gattaataaa ccgttattga ttccgttaaca tttaaacctt aatctaaattt 960
 atgagagccct ttgaaggagg tctggatgg aaaatttgaa gattagatat atagatacga 1020
 ggaagatagg aaccgtgagc ggtgtaaaag t 1051

<210> 126
<211> 305
<212> PRT
<213> Aquifex aeolicus

<400> 126

Met	Glu	Lys	Val	Phe	Leu	Glu	Lys	Leu	Gln	Lys	Thr	Leu	His	Ile	Pro
1				5				10						15	
Gly	Gly	Leu	Leu	Phe	Tyr	Gly	Lys	Glu	Gly	Ser	Gly	Lys	Thr	Lys	Thr
		20					25					30			
Ala	Phe	Glu	Phe	Ala	Lys	Gly	Ile	Leu	Cys	Lys	Glu	Asn	Val	Pro	Trp
				35			40					45			
Gly	Cys	Gly	Ser	Cys	Pro	Ser	Cys	Lys	His	Val	Asn	Glu	Leu	Glu	Glu
		50			55			60							
Ala	Phe	Phe	Lys	Gly	Glu	Ile	Glu	Asp	Phe	Lys	Val	Tyr	Lys	Asp	Lys
		65			70			75					80		
Asp	Gly	Lys	Lys	His	Phe	Val	Tyr	Leu	Met	Gly	Glu	His	Pro	Asp	Phe
		85				90				95					
Val	Val	Ile	Ile	Pro	Ser	Gly	His	Tyr	Ile	Lys	Ile	Glu	Gln	Ile	Arg
		100				105				110					
Glu	Val	Lys	Asn	Phe	Ala	Tyr	Val	Lys	Pro	Ala	Leu	Ser	Arg	Arg	Lys
		115				120				125					
Val	Ile	Ile	Ile	Asp	Asp	Ala	His	Ala	Met	Thr	Ser	Gln	Ala	Ala	Asn
		130			135				140						
Ala	Leu	Leu	Lys	Val	Leu	Glu	Glu	Pro	Pro	Ala	Asp	Thr	Thr	Phe	Ile
		145			150			155			160				
Leu	Thr	Thr	Asn	Arg	Arg	Ser	Ala	Ile	Leu	Pro	Thr	Ile	Leu	Ser	Arg
		165				170				175					
Thr	Phe	Gln	Val	Glu	Phe	Lys	Gly	Phe	Ser	Val	Lys	Glu	Val	Met	Glu
		180				185				190					
Ile	Ala	Lys	Val	Asp	Glu	Glu	Ile	Ala	Lys	Leu	Ser	Gly	Gly	Ser	Leu
		195				200				205					
Lys	Arg	Ala	Ile	Leu	Leu	Lys	Glu	Asn	Lys	Asp	Ile	Leu	Asn	Lys	Val
		210				215				220					

Lys Glu Phe Leu Glu Asn Glu Pro Leu Lys Val Tyr Lys Leu Ala Ser
225 230 235 240

Glu Phe Glu Lys Trp Glu Pro Glu Lys Gln Lys Leu Phe Leu Glu Ile
245 250 255

Met Glu Glu Leu Val Ser Gln Lys Leu Thr Glu Glu Lys Lys Asp Asn
260 265 270

Tyr Thr Tyr Leu Leu Asp Thr Ile Arg Leu Phe Lys Asp Gly Leu Ala
275 280 285

Arg Gly Val Asn Glu Pro Leu Trp Leu Phe Thr Leu Ala Val Gln Ala
290 295 300

Asp
305

<210> 127

<211> 630

<212> DNA

<213> Aquifex aeolicus

<400> 127
atgaacttcc tgaaaaagtt cctttactg agaaaagctc aaaagtctcc ttacttcgaa 60
gagttctacg aagaatcga ttgaaccag aaggtgaaag atgcaagggtt tggtagtttt 120
gactgcgaag ccacagaact cgacgtaaag aaggcaaaac tcctttcaat aggtgcgggtt 180
gaggtaaaa acctggaaat agacctctt aaatctttt acgagatact caaaagtgcac 240
gagataaagg cggcggagat acatggaata accagggaaag acgttgaaaa gtacggaaag 300
gaaccaaagg aagtaatata cgactttctg aagtacataa agggaaagcgt tctcggtggc 360
tactacgtga agtttgcgtt ctcactcggtt gagaagtact ccataaagta cttccagtt 420
ccaatcatca actacaagtt agacctgttt agtttcgtga agagagagta ccagagtggc 480
aggagtcttg acgaccttat gaaggaactc ggttagaaaa taaggcaag gcacaacgcc 540
cttgaagatg cctacataac cgctttttt ttccttaaagt acgtttaccc gaacagggag 600
tacagactaa aggtatctccc gattttcctt 630

<210> 128

<211> 210

<212> PRT

<213> Aquifex aeolicus

<400> 128
Met Asn Phe Leu Lys Lys Phe Leu Leu Arg Lys Ala Gln Lys Ser
1 5 10 15

Pro Tyr Phe Glu Glu Phe Tyr Glu Glu Ile Asp Leu Asn Gln Lys Val

20

25

30

Lys Asp Ala Arg Phe Val Val Phe Asp Cys Glu Ala Thr Glu Leu Asp
 35 40 45
 Val Lys Lys Ala Lys Leu Leu Ser Ile Gly Ala Val Glu Val Lys Asn
 50 55 60
 Leu Glu Ile Asp Leu Ser Lys Ser Phe Tyr Glu Ile Leu Lys Ser Asp
 65 70 75 80
 Glu Ile Lys Ala Ala Glu Ile His Gly Ile Thr Arg Glu Asp Val Glu
 85 90 95
 Lys Tyr Gly Lys Glu Pro Lys Glu Val Ile Tyr Asp Phe Leu Lys Tyr
 100 105 110
 Ile Lys Gly Ser Val Leu Val Gly Tyr Tyr Val Lys Phe Asp Val Ser
 115 120 125
 Leu Val Glu Lys Tyr Ser Ile Lys Tyr Phe Gln Tyr Pro Ile Ile Asn
 130 135 140
 Tyr Lys Leu Asp Leu Phe Ser Phe Val Lys Arg Glu Tyr Gln Ser Gly
 145 150 160
 Arg Ser Leu Asp Asp Leu Met Lys Glu Leu Gly Val Glu Ile Arg Ala
 165 170 175
 Arg His Asn Ala Leu Glu Asp Ala Tyr Ile Thr Ala Leu Leu Phe Leu
 180 185 190
 Lys Tyr Val Tyr Pro Asn Arg Glu Tyr Arg Leu Lys Asp Leu Pro Ile
 195 200 205
 Phe Leu
 210

<210> 129
 <211> 526
 <212> DNA
 <213> Aquifex aeolicus

<400> 129
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 ccgagcggaa cggccgtagt agagttact ctggcttaca acagaaggtt aaaaaaccag 120
 aacggtaat ttcaggagga aagtcaacttc tttgacgtaa aggcgtacgg aaaaatggct 180

gaagactggg ctacacgctt ctcgaaagga tacctcgta tcgttagaggg aagactctcc 240
caggaaaagt gggagaaaga agaaaagaag ttctcaaagg tcaggataat agcgaaaac 300
gtaagattaa taaacaggcc gaaagggtgc gaacttcaag cagaagaaga ggaggaagtt 360
cctccattg aggagggaaat tgaaaaactc ggtaaagagg aagagaagcc ttttaccgat 420
gaagaggacg aaataccctt ttaatttga ggaggttaaa gtatggtagt gagagctcct 480
aagaagaaag ttgtatgta ctgtgaacaa aagagagac cagatt 526

<210> 130

<211> 147

<212> PRT

<213> Aquifex aeolicus

<400> 130

Met Leu Asn Lys Val Phe Ile Ile Gly Arg Leu Thr Gly Asp Pro Val
1 5 10 15

Ile Thr Tyr Leu Pro Ser Gly Thr Pro Val Val Glu Phe Thr Leu Ala
20 25 30

Tyr Asn Arg Arg Tyr Lys Asn Gln Asn Gly Glu Phe Gln Glu Glu Ser
35 40 45

His Phe Phe Asp Val Lys Ala Tyr Gly Lys Met Ala Glu Asp Trp Ala
50 55 60

Thr Arg Phe Ser Lys Gly Tyr Leu Val Leu Val Glu Gly Arg Leu Ser
65 70 75 80

Gln Glu Lys Trp Glu Lys Glu Gly Lys Lys Phe Ser Lys Val Arg Ile
85 90 95

Ile Ala Glu Asn Val Arg Leu Ile Asn Arg Pro Lys Gly Ala Glu Leu
100 105 110

Gln Ala Glu Glu Glu Glu Val Pro Pro Ile Glu Glu Glu Ile Glu
115 120 125

Lys Leu Gly Lys Glu Glu Glu Lys Pro Phe Thr Asp Glu Glu Asp Glu
130 135 140

Ile Pro Phe

145

<210> 131

<211> 1472

<212> DNA

<213> Aquifex aeolicus

<400> 131

atgcaatttg tggataaact tccctgtgac gaatccgccg agagggcggt tcttggcagt 60
atgcttgaag accccgaaaa catacctctg gtacttgaat accttaaaga agaagacttc 120
tgcatacgacg agcacaagct acttttcagg gttcttacaa acctctggc cgagtagcgc 180
aataagctcg atttcgtatt aataaaggat caccttggaa agaaaaactt actccagaaa 240
atacctatacg actggctcga agaactctac gaggaggcgg tatcccctga cacgctttag 300
gaagtctgca aaatagtaaa acaacgttcc gcacagaggg cgataattca actcggtata 360
gaactcattc acaaaggaaa ggaaaacaaa gacttcaca cattaatcga ggaagccag 420
agcaggatata ttccatagc ggaaagtgtc acatctacgc agttttacca tgtgaaagac 480
gttgcggaaag aagttataga actcatttat aaattcaaaa gctctgacag gctagtcacg 540
ggactcccaa gcgtttcac ggaactcgat ctaaagacga cgggattcca ccctgagac 600
ttaataatac tcgcccgaag acccggtatg gggaaaaccc cctttatgtc ctccataatc 660
tacaatctcg caaaagacga gggaaaaccc tcagctgtat ttcccttggaa aatgagcaag 720
gaacagctcg ttatgagact cctctctatg atgtcggagg tcccactttt caagataagg 780
tcttggaaatgatcataatcga agatttaaag aagcttggaa agaactcgca 840
aagtacgaca tatacctcga cgacacaccc gctctacta caacggattt aaggataagg 900
gcaagaaagc tcagaaagga aaaggaagtt gagtcgtgg cgggtggacta cttgcaactt 960
ctgagaccgc cagtcgaaa gagttcaaga caggaggaag tggcagaggt ttcaagaaac 1020
ttaaaagccc ttgcaaagga acttcacatt cccgttatgg cacttgcgcgca gctctccgt 1080
gagggtggaaa agaggagtga taaaagaccc cagcttgcgg acctcagaga atccggacag 1140
atagaacagg accgacacct aatccttttc ctccacagac ccgagttacta caagaaaaag 1200
ccaaatcccg aagagcaggg tatacgccaa gtgataatag ccaagcaaag gcaaggaccc 1260
acggacattt tgaagctcgc atttattaaag gagttacta agtttgcggaa cctagaagcc 1320
cttccttgcac aacccttctga agaagagggaa ctttccggaa ttattgaaac acaggaggat 1380
gaaggattcg aagatattga cttctgaaaaa ttaagggtttt ataattttt cttggctatc 1440
cggggttagct caatcgccag agcgggtggc tg 1472

<210> 132

<211> 438

<212> PRT

<213> Aquifex aeolicus

<400> 132

Met Gln Phe Val Asp Lys Leu Pro Cys Asp Glu Ser Ala Glu Arg Ala

1 5 10 15

Val Leu Gly Ser Met Leu Glu Asp Pro Glu Asn Ile Pro Leu Val Leu

20 25 30

Glu Tyr Leu Lys Glu Glu Asp Phe Cys Ile Asp Glu His Lys Leu Leu

35 40 45

Phe Arg Val Leu Thr Asn Leu Trp Ser Glu Tyr Gly Asn Lys Leu Asp

50 55 60

Phe	Val	Leu	Ile	Lys	Asp	His	Leu	Glu	Lys	Asn	Leu	Leu	Gln	Lys	
65														80	
Ile	Pro	Ile	Asp	Trp	Leu	Glu	Glu	Leu	Tyr	Glu	Ala	Val	Ser	Pro	
														95	
Asp	Thr	Leu	Glu	Glu	Val	Cys	Lys	Ile	Val	Lys	Gln	Arg	Ser	Ala	Gln
														110	
Arg	Ala	Ile	Ile	Gln	Leu	Gly	Ile	Thr	Ser	Thr	Gln	Phe	Tyr	His	Val
o														125	
Lys	Asp	Val	Ala	Glu	Glu	Val	Ile	Glu	Leu	Ile	Tyr	Lys	Phe	Lys	Ser
														140	
Ser	Asp	Arg	Leu	Val	Thr	Gly	Leu	Pro	Ser	Gly	Phe	Thr	Glu	Leu	Asp
145														160	
Leu	Lys	Thr	Thr	Gly	Phe	His	Pro	Gly	Asp	Leu	Ile	Ile	Leu	Ala	Ala
														175	
Arg	Pro	Gly	Met	Gly	Lys	Thr	Ala	Phe	Met	Leu	Ser	Ile	Ile	Tyr	Asn
														190	
Leu	Ala	Lys	Asp	Glu	Gly	Lys	Pro	Ser	Ala	Val	Phe	Ser	Leu	Glu	Met
														205	
Ser	Lys	Glu	Gln	Leu	Val	Met	Arg	Leu	Leu	Ser	Met	Met	Ser	Glu	Val
														220	
Pro	Leu	Phe	Lys	Ile	Arg	Ser	Gly	Ser	Ile	Ser	Asn	Glu	Asp	Leu	Lys
225														240	
Lys	Leu	Glu	Ala	Ser	Ala	Ile	Glu	Leu	Ala	Lys	Tyr	Asp	Ile	Tyr	Leu
														255	
Asp	Asp	Thr	Pro	Ala	Leu	Thr	Thr	Asp	Leu	Arg	Ile	Arg	Ala	Arg	
														270	
Lys	Leu	Arg	Lys	Glu	Lys	Glu	Val	Glu	Phe	Val	Ala	Val	Asp	Tyr	Leu
														285	
Gln	Leu	Leu	Arg	Pro	Pro	Val	Arg	Lys	Ser	Ser	Arg	Gln	Glu	Glu	Val
														300	
Ala	Glu	Val	Ser	Arg	Asn	Leu	Lys	Ala	Leu	Lys	Glu	Leu	His	Ile	
305														320	

Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu Ser Gly Gln Ile Glu
340 345 350

Gln Asp Ala Asp Leu Ile Leu Phe Leu His Arg Pro Glu Tyr Tyr Lys
 355 360 365

Lys Lys Pro Asn Pro Glu Glu Gln Gly Ile Ala Glu Val Ile Ile Ala
370 375 380

Lys Gln Arg Gln Gly Pro Thr Asp Ile Val Lys Leu Ala Phe Ile Lys
 385 390 395 400

Glu Tyr Thr Lys Phe Ala Asn Leu Glu Ala Leu Pro Glu Gln Pro Pro
405 410 415

Glu Glu Glu Glu Leu Ser Glu Ile Ile Glu Thr Gln Glu Asp Glu Gly
 420 425 430

Phe Glu Asp Ile Asp Phe
435

<210> 133
<211> 1526
<212> DNA
<213> *Aquifex aeolicus*

<400> 133
atgtcctcgg acatagacga acttagacgg gaaatagata tagtagacgt catttccgaa 60
tacttaaact tagagaaggtagt aggttccaat tacagaacga actgtccctt tcaccctgac 120
gatacaccct cctttacgt gtctccaagt aaacaaatat tcaagtgttt cggttgccggg 180
gtagggggag acgcgataaa gttcgttcc ctttacgagg acatctccta ttttgaagcc 240
gcccttgaac tcgcaaaacg ctacgaaaag aaatttagacc ttgaaaagat atcaaaaagac 300
gaaaaggat acgtggctct tgacagggtt tgtgatttct acagggaaag cttctcaaa 360
aacagagagg caagtgagta cgtaaagagt aggggaatag accctaaagt agcgaggaag 420
tttgatcttg ggtacgcacc ttccagtgaa gcactcgtaa aagtcttaaa agagaacgat 480
cttttagagg cttaaccttga aactaaaaac ctcccttctc ctacgaaggg tgtttacagg 540
gatctcttcc ttccggcgtgt cgtgatccccg ataaaggatc cgagggaaag agttataaggt 600
ttcgggtggaa ggaggatagt agaggacaaa tctcccaagt acataaaactc tccagacagc 660
agggtattta aaaagggggaa gaacttattc ggtcttacg aggcaaagga gtatataaaag 720
gaagaaggat ttgcgataact tgtgaaaggg tactttgacc ttttgagact ttttccgag 780
ggaataagga acgttgtgc acccctcggt acagccctga cccaaaatca ggcaaacctc 840
ctttcccaagt tcacaaaaaaa ggtctacatc cttaacgacg gagatgatgc gggaaagaaag 900
gctatgaaaaa gtgcattcc cctactcctc agtgcaggag tggaagtttaccccgttac 960
ctcccccaag gatacgatcc cgacgagttt ataaaggaat tcggaaaga ggaattaaga 1020

agactgataa acagctcagg ggagctctt gaaacgctca taaaaaccgc aaggaaaaac 1080
ttagaggaga aaacgcgtga gttcaggtat tatctgggct ttatccga tggagtaagg 1140
cgcttgctc tggcttcgga gttcacacc aagtacaaag ttcctatgga aattttatta 1200
atgaaaattg aaaaaaattc tcaagaaaaa gaaattaaac ttcctttaa ggaaaaaattc 1260
ttcctgaaag gactgataga attaaaacca aaaatagacc ttgaagtcct gaacttaagt 1320
cctgagttaa aggaactcgc agttaacgcc ttaaacggag aggagcatt acttccaaaa 1380
gaagttctcg agtaccaggt ggataacttg gagaaacttt ttaacaacat ccttagggat 1440
ttacaaaaat ctgggaaaaa gaggaagaaa agagggttga aaaatgtaaa tacttaatta 1500
acttaataa attttagag tttagga 1526

<210> 134

<211> 498

<212> PRT

<213> Aquifex aeolicus

<400> 134

Met Ser Ser Asp Ile Asp Glu Leu Arg Arg Glu Ile Asp Ile Val Asp
1 5 10 15

Val Ile Ser Glu Tyr Leu Asn Leu Glu Lys Val Gly Ser Asn Tyr Arg
20 25 30

Thr Asn Cys Pro Phe His Pro Asp Asp Thr Pro Ser Phe Tyr Val Ser
35 40 45

Pro Ser Lys Gln Ile Phe Lys Cys Phe Gly Cys Gly Val Gly Gly Asp
50 55 60

Ala Ile Lys Phe Val Ser Leu Tyr Glu Asp Ile Ser Tyr Phe Glu Ala
65 70 75 80

Ala Leu Glu Leu Ala Lys Arg Tyr Gly Lys Lys Leu Asp Leu Glu Lys
85 90 95

Ile Ser Lys Asp Glu Lys Val Tyr Val Ala Leu Asp Arg Val Cys Asp
100 105 110

Phe Tyr Arg Glu Ser Leu Leu Lys Asn Arg Glu Ala Ser Glu Tyr Val
115 120 125

Lys Ser Arg Gly Ile Asp Pro Lys Val Ala Arg Lys Phe Asp Leu Gly
130 135 140

Tyr Ala Pro Ser Ser Glu Ala Leu Val Lys Val Leu Lys Glu Asn Asp
145 150 155 160

Leu Leu Glu Ala Tyr Leu Glu Thr Lys Asn Leu Leu Ser Pro Thr Lys

165

170

175

Gly Val Tyr Arg Asp Leu Phe Leu Arg Arg Val Val Ile Pro Ile Lys
 180 185 190

Asp Pro Arg Gly Arg Val Ile Gly Phe Gly Gly Arg Arg Ile Val Glu
 195 200 205

Asp Lys Ser Pro Lys Tyr Ile Asn Ser Pro Asp Ser Arg Val Phe Lys
 210 215 220

Lys Gly Glu Asn Leu Phe Gly Leu Tyr Glu Ala Lys Glu Tyr Ile Lys
 225 230 235 240

Glu Glu Gly Phe Ala Ile Leu Val Glu Gly Tyr Phe Asp Leu Leu Arg
 245 250 255

Leu Phe Ser Glu Gly Ile Arg Asn Val Val Ala Pro Leu Gly Thr Ala
 260 265 270

Leu Thr Gln Asn Gln Ala Asn Leu Leu Ser Lys Phe Thr Lys Lys Val
 275 280 285

Tyr Ile Leu Tyr Asp Gly Asp Asp Ala Gly Arg Lys Ala Met Lys Ser
 290 295 300

Ala Ile Pro Leu Leu Ser Ala Gly Val Glu Val Tyr Pro Val Tyr
 305 310 315 320

Leu Pro Glu Gly Tyr Asp Pro Asp Glu Phe Ile Lys Glu Phe Gly Lys
 325 330 335

Glu Glu Leu Arg Arg Leu Ile Asn Ser Ser Gly Glu Leu Phe Glu Thr
 340 345 350

Leu Ile Lys Thr Ala Arg Glu Asn Leu Glu Glu Lys Thr Arg Glu Phe
 355 360 365

Arg Tyr Tyr Leu Gly Phe Ile Ser Asp Gly Val Arg Arg Phe Ala Leu
 370 375 380

Ala Ser Glu Phe His Thr Lys Tyr Lys Val Pro Met Glu Ile Leu Leu
 385 390 395 400

Met Lys Ile Glu Lys Asn Ser Gln Glu Lys Glu Ile Lys Leu Ser Phe
 405 410 415

Lys Glu Lys Ile Phe Leu Lys Gly Leu Ile Glu Leu Lys Pro Lys Ile

420

425

430

Asp Leu Glu Val Leu Asn Leu Ser Pro Glu Leu Lys Glu Leu Ala Val
435 440 445

Asn Ala Leu Asn Gly Glu Glu His Leu Leu Pro Lys Glu Val Leu Glu
450 455 460

Tyr Gln Val Asp Asn Leu Glu Lys Leu Phe Asn Asn Ile Leu Arg Asp
465 470 475 480

Leu Gln Lys Ser Gly Lys Lys Arg Lys Lys Arg Gly Leu Lys Asn Val
485 490 495

Asn Thr

<210> 135

<211> 705

<212> DNA

<213> Aquifex aeolicus

<400> 135

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aacaaggtaa ggctctgcga atgcaggttc aagaaaaggg atgtaaacag ggaactaaac 120
atcccaaaga ggtactggaa cgccaaactta gacacttacc accccaagaa cgtatcccag 180
aacagggcac ttttgcacat aagggtcttc gtccacaact tcaatcccga ggaagggaaa 240
gggcttacct ttgttaggatc tcctggagtc ggcaaaaactc accttgcgggt tgcaacattt 300
aaagcgattt atgagaagaa gggaaatcaga ggataacttct tcgatacggaa ggatctaata 360
ttcaggtaa aacacttaat ggacgaggga aaggatacaa agtttttaaa aactgtctta 420
aactcaccgg ttttggttct cgacgacctc ggttctgaga ggctcagtga ctggcagagg 480
gaactcatct cttacataat cacttacagg tataacaacc ttaagagcac gataataacc 540
acgaattact cactccagag ggaagaagag agtagcgtga ggataagtgc ggatcttgca 600
agcagactcg gagaaaacgt agtttcaaaa atttacgaga tgaacgagtt gctcgttata 660
aagggttccg acctcaggaa gtctaaaaag ctatcaaccc catct 705

<210> 136

<211> 235

<212> PRT

<213> Aquifex aeolicus

<400> 136

Met Gln Asp Thr Ala Thr Cys Ser Ile Cys Gln Gly Thr Gly Phe Val
1 5 10 15

Lys Thr Glu Asp Asn Lys Val Arg Leu Cys Glu Cys Arg Phe Lys Lys

20

25

30

Arg Asp Val Asn Arg Glu Leu Asn Ile Pro Lys Arg Tyr Trp Asn Ala
 35 40 45

Asn Leu Asp Thr Tyr His Pro Lys Asn Val Ser Gln Asn Arg Ala Leu
 50 55 60

Leu Thr Ile Arg Val Phe Val His Asn Phe Asn Pro Glu Glu Gly Lys
 65 70 75 80

Gly Leu Thr Phe Val Gly Ser Pro Gly Val Gly Lys Thr His Leu Ala
 85 90 95

Val Ala Thr Leu Lys Ala Ile Tyr Glu Lys Lys Gly Ile Arg Gly Tyr
 100 105 110

Phe Phe Asp Thr Lys Asp Leu Ile Phe Arg Leu Lys His Leu Met Asp
 115 120 125

Glu Gly Lys Asp Thr Lys Phe Leu Lys Thr Val Leu Asn Ser Pro Val
 130 135 140

Leu Val Leu Asp Asp Leu Gly Ser Glu Arg Leu Ser Asp Trp Gln Arg
 145 150 155 160

Glu Leu Ile Ser Tyr Ile Ile Thr Tyr Arg Tyr Asn Asn Leu Lys Ser
 165 170 175

Thr Ile Ile Thr Thr Asn Tyr Ser Leu Gln Arg Glu Glu Ser Ser
 180 185 190

Val Arg Ile Ser Ala Asp Leu Ala Ser Arg Leu Gly Glu Asn Val Val
 195 200 205

Ser Lys Ile Tyr Glu Met Asn Glu Leu Leu Val Ile Lys Gly Ser Asp
 210 215 220

Leu Arg Lys Ser Lys Lys Leu Ser Thr Pro Ser
 225 230 235

<210> 137

<211> 4101

<212> DNA

<213> *Thermatoga maritima*

<400> 137

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gtgcgttac tggagaagaa gacgcggttt cgagtcatcg tgaacgggt tcaaaaaagt 180
aacggggatc taaggggaaa gatacttcc cttctcaacg gtaatgtgcc ttacataaaa 240
gatgttggtt tcgaaggaaa caggctgatt ctgaaagtgc ttggagatt cgccgggac 300
aggatgcct ccaaactcag aagcacgaaa aaacagctcg atgaactgct gcctcccgga 360
acagagatca tgctggaggt tggaggtt ccggaagatc tttgaaaaaa ggaagtagcca 420
caaccagaaa agagagaaga accaaagggt gaagaattga agatcgagga tgaaaaccac 480
atcttggac agaaaccag aaagatcgtc ttcacccct caaaatctt tgagtacaac 540
aaaaagacat cggtaaggg caagatcttcaaaatagaga agatcgaggg gaaaagaacg 600
gtccttctga tttacctgac agacggagaa gattctctga tctgaaatgt cttcaacgac 660
tttggaaaagg tcgaaggaaa agtacgggtt ggagacgtga tcgttgcac aggagacctc 720
cttctgaaa acggggagcc cacccttac gtgaaggaa tcacaaaact tccgaagcg 780
aaaaggatgg acaaacttcc ggttaagagg gtggagctcc acgcccatac caagttcagc 840
gatcaggacg caataacaga tggtaacgaa tatgtgaaac gagccaagga atggggctt 900
cccgatcgatcc ccctcacgga tcatggaaac gttcaggcca taccttactt ctacgacgac 960
gcaaaagaag ctgaaataaa gcccatttc ggtatcgaag cgtatctggt gagtgacgtg 1020
gagccgtca taaggaatct ctccgacgat tcgacgtttt gagatgccac gttcgctgc 1080
ctcgacttcg agacgacggg ttcgaccccg caggtggatg agatcatcgat gataggagcg 1140
gtgaagatac agggtggcca gatagtggac ggttaccata ctctcataaa gccttccagg 1200
gagatctcaa gaaaaagttc ggagatcacc ggaatcactc aagagatgct gaaaaacaag 1260
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ttggactggg aaagacccta catagatacg ctgccttcg caaagtcctt tctcaaactg 1440
agaagctact ctctggatttgc cgttggaa aagctcgat tgggtccctt ccggcaccac 1500
agggccctgg atgacgacgg ggtcaccgtt caggtttcc tcaggttgc tgagatgtat 1560
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<210> 138

<211> 1367

<212> PRT

<213> *Thermatoga maritima*

<400> 138

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															15

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															30

Phe	Ser	Glu	Glu	Ile	Glu	Asp	Leu	Val	Arg	Leu	Leu	Glu	Lys	Thr	
															45

Arg	Phe	Arg	Val	Ile	Val	Asn	Gly	Val	Gln	Lys	Ser	Asn	Gly	Asp	Leu
															50
															55
															60

Arg	Gly	Lys	Ile	Leu	Ser	Leu	Leu	Asn	Gly	Asn	Val	Pro	Tyr	Ile	Lys
															65
															70
															75
															80

Asp	Val	Val	Phe	Glu	Gly	Asn	Arg	Leu	Ile	Leu	Lys	Val	Leu	Gly	Asp
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															90
															95

Phe Ala Arg Asp Arg Ile Ala Ser Lys Leu Arg Ser Thr Lys Gln

100 105 110
Leu Asp Glu Leu Leu Pro Pro Gly Thr Glu Ile Met Leu Glu Val Val
115 120 125
Glu Pro Pro Glu Asp Leu Leu Lys Lys Glu Val Pro Gln Pro Glu Lys
130 135 140
Arg Glu Glu Pro Lys Gly Glu Glu Leu Lys Ile Glu Asp Glu Asn His
145 150 155 160
Ile Phe Gly Gln Lys Pro Arg Lys Ile Val Phe Thr Pro Ser Lys Ile
165 170 175
Phe Glu Tyr Asn Lys Lys Thr Ser Val Lys Gly Lys Ile Phe Lys Ile
180 185 190
Glu Lys Ile Glu Gly Lys Arg Thr Val Leu Leu Ile Tyr Leu Thr Asp
195 200 205
Gly Glu Asp Ser Leu Ile Cys Lys Val Phe Asn Asp Val Glu Lys Val
210 215 220
Glu Gly Lys Val Ser Val Gly Asp Val Ile Val Ala Thr Gly Asp Leu
225 230 235 240
Leu Leu Glu Asn Gly Glu Pro Thr Leu Tyr Val Lys Gly Ile Thr Lys
245 250 255
Leu Pro Glu Ala Lys Arg Met Asp Lys Ser Pro Val Lys Arg Val Glu
260 265 270
Leu His Ala His Thr Lys Phe Ser Asp Gln Asp Ala Ile Thr Asp Val
275 280 285
Asn Glu Tyr Val Lys Arg Ala Lys Glu Trp Gly Phe Pro Ala Ile Ala
290 295 300
Leu Thr Asp His Gly Asn Val Gln Ala Ile Pro Tyr Phe Tyr Asp Ala
305 310 315 320
Ala Lys Glu Ala Gly Ile Lys Pro Ile Phe Gly Ile Glu Ala Tyr Leu
325 330 335
Val Ser Asp Val Glu Pro Val Ile Arg Asn Leu Ser Asp Asp Ser Thr
340 345 350
Phe Gly Asp Ala Thr Phe Val Val Leu Asp Phe Glu Thr Thr Gly Leu

355

360

365

Asp Pro Gln Val Asp Glu Ile Ile Glu Ile Gly Ala Val Lys Ile Gln
 370 375 380
 Gly Gly Gln Ile Val Asp Glu Tyr His Thr Leu Ile Lys Pro Ser Arg
 385 390 395 400
 Glu Ile Ser Arg Lys Ser Ser Glu Ile Thr Gly Ile Thr Gln Glu Met
 405 410 415
 Leu Glu Asn Lys Arg Ser Ile Glu Glu Val Leu Pro Glu Phe Leu Gly
 420 425 430
 Phe Leu Glu Asp Ser Ile Ile Val Ala His Asn Ala Asn Phe Asp Tyr
 435 440 445
 Arg Phe Leu Arg Leu Trp Ile Lys Lys Val Met Gly Leu Asp Trp Glu
 450 455 460
 Arg Pro Tyr Ile Asp Thr Leu Ala Leu Ala Lys Ser Leu Leu Lys Leu
 465 470 475 480
 Arg Ser Tyr Ser Leu Asp Ser Val Val Glu Lys Leu Gly Leu Gly Pro
 485 490 495
 Phe Arg His His Arg Ala Leu Asp Asp Ala Arg Val Thr Ala Gln Val
 500 505 510
 Phe Leu Arg Phe Val Glu Met Met Lys Lys Ile Gly Ile Thr Lys Leu
 515 520 525
 Ser Glu Met Glu Lys Leu Lys Asp Thr Ile Asp Tyr Thr Ala Leu Lys
 530 535 540
 Pro Phe His Cys Thr Ile Leu Val Gln Asn Lys Lys Gly Leu Lys Asn
 545 550 555 560
 Leu Tyr Lys Leu Val Ser Asp Ser Tyr Ile Lys Tyr Phe Tyr Gly Val
 565 570 575
 Pro Arg Ile Leu Lys Ser Glu Leu Ile Glu Asn Arg Glu Gly Leu Leu
 580 585 590
 Val Gly Ser Ala Cys Ile Ser Gly Glu Leu Gly Arg Ala Ala Leu Glu
 595 600 605
 Gly Ala Ser Asp Ser Glu Leu Glu Glu Ile Ala Lys Phe Tyr Asp Tyr

610 615 620
Ile Glu Val Met Pro Leu Asp Val Ile Ala Glu Asp Glu Glu Asp Leu
625 630 635 640
Asp Arg Glu Arg Leu Lys Glu Val Tyr Arg Lys Leu Tyr Arg Ile Ala
645 650 655
Lys Lys Leu Asn Lys Phe Val Val Met Thr Gly Asp Val His Phe Leu
660 665 670
Asp Pro Glu Asp Ala Arg Gly Arg Ala Ala Leu Leu Ala Pro Gln Gly
675 680 685
Asn Arg Asn Phe Glu Asn Gln Pro Ala Leu Tyr Leu Arg Thr Thr Glu
690 695 700
Glu Met Leu Glu Lys Ala Ile Glu Ile Phe Glu Asp Glu Glu Ile Ala
705 710 715 720
Arg Glu Val Val Ile Glu Asn Pro Asn Arg Ile Ala Asp Met Ile Glu
725 730 735
Glu Val Gln Pro Leu Glu Lys Lys Leu His Pro Pro Ile Ile Glu Asn
740 745 750
Ala Asp Glu Ile Val Arg Asn Leu Thr Met Lys Arg Ala Tyr Glu Ile
755 760 765
Tyr Gly Asp Pro Leu Pro Glu Ile Val Gln Lys Arg Val Glu Lys Glu
770 775 780
Leu Asn Ala Ile Ile Asn His Gly Tyr Ala Val Leu Tyr Leu Ile Ala
785 790 795 800
Gln Glu Leu Val Gln Lys Ser Met Ser Asp Gly Tyr Val Val Gly Ser
805 810 815
Arg Gly Ser Val Gly Ser Ser Leu Val Ala Asn Leu Leu Gly Ile Thr
820 825 830
Glu Val Asn Pro Leu Pro Pro His Tyr Arg Cys Pro Glu Cys Lys Tyr
835 840 845
Phe Glu Val Val Glu Asp Asp Arg Tyr Gly Ala Gly Tyr Asp Leu Pro
850 855 860
Asn Lys Asn Cys Pro Arg Cys Gly Ala Pro Leu Arg Lys Asp Gly His

865	870	875	880
Gly Ile Pro Phe Glu Thr Phe Met Gly Phe Glu Gly Asp Lys Val Pro			
885	890	895	
Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Glu Arg Ala His Arg			
900	905	910	
Phe Val Glu Glu Leu Phe Gly Lys Asp His Val Tyr Arg Ala Gly Thr			
915	920	925	
Ile Asn Thr Ile Ala Glu Arg Ser Ala Val Gly Tyr Val Arg Ser Tyr			
930	935	940	
Glu Glu Lys Thr Gly Lys Lys Leu Arg Lys Ala Glu Met Glu Arg Leu			
945	950	955	960
Val Ser Met Ile Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro Gly			
965	970	975	
Gly Leu Met Ile Ile Pro Lys Asp Lys Glu Val Tyr Asp Phe Thr Pro			
980	985	990	
Ile Gln Tyr Pro Ala Asn Asp Arg Asn Ala Gly Val Phe Thr Thr His			
995	1000	1005	
Phe Ala Tyr Glu Thr Ile His Asp Asp Leu Val Lys Ile Asp Ala Leu			
1010	1015	1020	
Gly His Asp Asp Pro Thr Phe Ile Lys Met Leu Lys Asp Leu Thr Gly			
1025	1030	1035	1040
Ile Asp Pro Met Thr Ile Pro Met Asp Asp Pro Asp Thr Leu Ala Ile			
1045	1050	1055	
Phe Ser Ser Val Lys Pro Leu Gly Val Asp Pro Val Glu Leu Glu Ser			
1060	1065	1070	
Asp Val Gly Thr Tyr Gly Ile Pro Glu Phe Gly Thr Glu Phe Val Arg			
1075	1080	1085	
Gly Met Leu Val Glu Thr Arg Pro Lys Ser Phe Ala Glu Leu Val Arg			
1090	1095	1100	
Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Asn Asn Ala Arg			
1105	1110	1115	1120
Asp Trp Ile Asn Leu Gly Tyr Ala Lys Leu Ser Glu Val Ile Ser Cys			

1125 1130 1135
Arg Asp Asp Ile Met Asn Phe Leu Ile His Lys Gly Met Glu Pro Ser
1140 1145 1150
Leu Ala Phe Lys Ile Met Glu Asn Val Arg Lys Gly Lys Gly Ile Thr
1155 1160 1165
Glu Glu Met Glu Ser Glu Met Arg Arg Leu Lys Val Pro Glu Trp Phe
1170 1175 1180
Ile Glu Ser Cys Lys Arg Ile Lys Tyr Leu Phe Pro Lys Ala His Ala
1185 1190 1195 1200
Val Ala Tyr Val Ser Met Ala Phe Arg Ile Ala Tyr Phe Lys Val His
1205 1210 1215
Tyr Pro Leu Gln Phe Tyr Ala Ala Tyr Phe Thr Ile Lys Gly Asp Gln
1220 1225 1230
Phe Asp Pro Val Leu Val Leu Arg Gly Lys Glu Ala Ile Lys Arg Arg
1235 1240 1245
Leu Arg Glu Leu Lys Ala Met Pro Ala Lys Asp Ala Gln Lys Lys Asn
1250 1255 1260
Glu Val Ser Val Leu Glu Val Ala Leu Glu Met Ile Leu Arg Gly Phe
1265 1270 1275 1280
Ser Phe Leu Pro Pro Asp Ile Phe Lys Ser Asp Ala Lys Lys Phe Leu
1285 1290 1295
Ile Glu Gly Asn Ser Leu Arg Ile Pro Phe Asn Lys Leu Pro Gly Leu
1300 1305 1310
Gly Asp Ser Val Ala Glu Ser Ile Ile Arg Ala Arg Glu Glu Lys Pro
1315 1320 1325
Phe Thr Ser Val Glu Asp Leu Met Lys Arg Thr Lys Val Asn Lys Asn
1330 1335 1340
His Ile Glu Leu Met Lys Ser Leu Gly Val Leu Gly Asp Leu Pro Glu
1345 1350 1355 1360
Thr Glu Gln Phe Thr Leu Phe
1365

<210> 139
<211> 567
<212> DNA
<213> Thermatoga maritima

<400> 139
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accgatccct ttgccggaga ccggatagtt gaaatagccg ctgttcctgt cttcaagggg 120
aagatctaca gaaacaaagc gtttcactct ctcgtgaatc ccagaataag aatccctgcg 180
ctgattcaga aagttcacgg tattcagcaac atggacatcg tggaaagcgcc agacatggac 240
acagtttacg atctttcag ggattacgtg aaggaaacgg tgctcgtgtt tcacaacgcc 300
aacttcgacc tcactttct ggatatgtg gcaaagaaa cgggaaactt tccaataacg 360
aattccctaca tcgacacact cgatcttca gaagagatct ttggaaggcc tcattcttc 420
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gccctggtaa ccgcaagagt ttttgtgaag cttgttaat ttcttggtaa aaacagggtc 540
567
aacgaattca tacgtggaaa acgggggg

<210> 140
<211> 189
<212> PRT
<213> Thermatoga maritima

<400> 140
Met Leu Ala Met Ile Trp Asn Asp Thr Val Phe Cys Val Val Asp Thr
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Glu Thr Thr Gly Thr Asp Pro Phe Ala Gly Asp Arg Ile Val Glu Ile
20 25 30
Ala Ala Val Pro Val Phe Lys Gly Lys Ile Tyr Arg Asn Lys Ala Phe
35 40 45
His Ser Leu Val Asn Pro Arg Ile Arg Ile Pro Ala Leu Ile Gln Lys
50 55 60
Val His Gly Ile Ser Asn Met Asp Ile Val Glu Ala Pro Asp Met Asp
65 70 75 80
Thr Val Tyr Asp Leu Phe Arg Asp Tyr Val Lys Gly Thr Val Leu Val
85 90 95
Phe His Asn Ala Asn Phe Asp Leu Thr Phe Leu Asp Met Met Ala Lys
100 105 110
Glu Thr Gly Asn Phe Pro Ile Thr Asn Pro Tyr Ile Asp Thr Leu Asp
115 120 125

Leu Ser Glu Glu Ile Phe Gly Arg Pro His Ser Leu Lys Trp Leu Ser
130 135 140

Glu Arg Leu Gly Ile Lys Thr Thr Ile Arg His Arg Ala Leu Pro Asp
145 150 155 160

Ala Leu Val Thr Ala Arg Val Phe Val Lys Leu Val Glu Phe Leu Gly
165 170 175

Glu Asn Arg Val Asn Glu Phe Ile Arg Gly Lys Arg Gly
180 185

<210> 141

<211> 1434

<212> DNA

<213> Thermatoga maritima

<400> 141

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ttcgccggtc cgaggggAAC gggaaagact actcttgcca gaattctcgc aaaatccctg 180
aactgtgaga acagaaaggg agttgaaccc tgcaattcct gcagagcctg cagagagata 240
gacgagggaa cttcatgga cgtgatagag ctcgacgcgg cctccaacag aggaatagac 300
gagatcagaa gaatcagaga cggcgttggta tacaggccga tggaaaggtaa atacaaaagtc 360
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ctcgaagaac ctcccccac cgtcgtgttc gtgctggaa cgacaaacct tgagaaggaa 480
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atcgaaaaga ggctccagga agttgcggag gctgaaggaa tagagataga cagggaaagct 600
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atttttctta gaaaactcgg gaaaaaagta gaagttgaac ttgcactgat gggaaaagaa 1380
gaaaacaatcg agaaggtttc tcagaagatc ctgagattgt ttgaacagga gggaa 1434

<210> 142

<211> 478

<212> PRT

<213> Thermatoga maritima

<400> 142
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20 25 30
Asn Ser Val Ala His Gly Tyr Ile Phe Ala Gly Pro Arg Gly Thr Gly
35 40 45
Lys Thr Thr Leu Ala Arg Ile Leu Ala Lys Ser Leu Asn Cys Glu Asn
50 55 60
Arg Lys Gly Val Glu Pro Cys Asn Ser Cys Arg Ala Cys Arg Glu Ile
65 70 75 80
Asp Glu Gly Thr Phe Met Asp Val Ile Glu Leu Asp Ala Ala Ser Asn
85 90 95
Arg Gly Ile Asp Glu Ile Arg Arg Ile Arg Asp Ala Val Gly Tyr Arg
100 105 110
Pro Met Glu Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Val His Met
115 120 125
Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro
130 135 140
Pro Ser His Val Val Phe Val Leu Ala Thr Thr Asn Leu Glu Lys Val
145 150 155 160
Pro Pro Thr Ile Ile Ser Arg Cys Gln Val Phe Glu Phe Arg Asn Ile
165 170 175
Pro Asp Glu Leu Ile Glu Lys Arg Leu Gln Glu Val Ala Glu Ala Glu
180 185 190
Gly Ile Glu Ile Asp Arg Glu Ala Leu Ser Phe Ile Ala Lys Arg Ala
195 200 205
Ser Gly Gly Leu Arg Asp Ala Leu Thr Met Leu Glu Gln Val Trp Lys
210 215 220
Phe Ser Glu Gly Lys Ile Asp Leu Glu Thr Val His Arg Ala Leu Gly
225 230 235 240

Leu Ile Pro Ile Gln Val Val Arg Asp Tyr Val Asn Ala Ile Phe Ser
 245 250 255
 Gly Asp Val Lys Arg Val Phe Thr Val Leu Asp Asp Val Tyr Tyr Ser
 260 265 270
 Gly Lys Asp Tyr Glu Val Leu Ile Gln Glu Ala Val Glu Asp Leu Val
 275 280 285
 Glu Asp Leu Glu Arg Glu Arg Gly Val Tyr Gln Val Ser Ala Asn Asp
 290 295 300
 Ile Val Gln Val Ser Arg Gln Leu Leu Asn Leu Leu Arg Glu Ile Lys
 305 310 315 320
 Phe Ala Glu Glu Lys Arg Leu Val Cys Lys Val Gly Ser Ala Tyr Ile
 325 330 335
 Ala Thr Arg Phe Ser Thr Thr Asn Val Gln Glu Asn Asp Val Arg Glu
 340 345 350
 Lys Asn Asp Asn Ser Asn Val Gln Gln Lys Glu Glu Lys Lys Glu Thr
 355 360 365
 Val Lys Ala Lys Glu Glu Lys Gln Glu Asp Ser Glu Phe Glu Lys Arg
 370 375 380
 Phe Lys Glu Leu Met Glu Glu Leu Lys Glu Lys Gly Asp Leu Ser Ile
 385 390 395 400
 Phe Val Ala Leu Ser Leu Ser Glu Val Gln Phe Asp Gly Glu Lys Val
 405 410 415
 Ile Ile Ser Phe Asp Ser Ser Lys Ala Met His Tyr Glu Leu Met Lys
 420 425 430
 Lys Lys Leu Pro Glu Leu Glu Asn Ile Phe Ser Arg Lys Leu Gly Lys
 435 440 445
 Lys Val Glu Val Glu Leu Arg Leu Met Gly Lys Glu Glu Thr Ile Glu
 450 455 460
 Lys Val Ser Gln Lys Ile Leu Arg Leu Phe Glu Gln Glu Gly
 465 470 475

<210> 143
 <211> 1098

<212> DNA

<213> *Thermatoga maritima*

<400> 143

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ctcgaaaga aatccgtgaa acccatttt gctggatttc ttttgcagaat gaaagatgga 120
aatttctaca tctgcgcgac cgatctcgag accggagtca aagcaaccgt gaatgccgct 180
gaaatctccg gtgagggcagc ttttgcggta ccagggatgc tcattcagaa gatggtaaag 240
gttctcccg atgagataac ggaactttct ttagaggggg atgctttgt tataagttct 300
ggaagcaccg ttttcaggat caccaccatg cccgcggacg aatttccaga gataacgcct 360
gccgagtctg gaataaacctt cgaagttgac acttcgctcc tcgaggaaat ggttggaaag 420
gtcatcttcg ccgcgtccaa agacgagttc atgcgaaatc tgaatggagt tttctggaa 480
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gagcagatag aaaacgagga agaggcggat ttcttgctct ctttgcggatg catggaaagaa 600
gttcaaaacg tgctggacaa cacaacggag ccgactataa cggtgaggtt cgtggaaaga 660
agggtttctc tgtcgacaaa tgatgttagaa acggtgatga gagtggttcga cgctgaaattt 720
cccgattaca aaagggtgat ccccgaaact ttcaaaacga aagtgggtgtt ttccagaaaa 780
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aagttcgaaa tagaagaaaa cggttatgaga cttgtgagca agagccccgaa ttatggagaa 900
gtggtcgtatg aagtgcgttgc tcaaaaagaa gggaaagatc tcgtgatcgc tttcaacccg 960
aagttcatcg aggacgtttt gaagcacatt gagactgaag aaatcgaaat gaacttcgtt 1020
gattctacca gtccatgtca gataaatcca ctcgatattt ctggataccct ttacatagtg 1080
atgcccattca gactggca 1098

<210> 144

<211> 366

<212> PRT

<213> *Thermatoga maritima*

<400> 144

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1

5

10

15

Ala Ser Lys Ala Leu Ala Lys Lys Ser Val Lys Pro Ile Leu Ala Gly

20

25

30

Phe Leu Phe Glu Val Lys Asp Gly Asn Phe Tyr Ile Cys Ala Thr Asp

35

40

45

Leu Glu Thr Gly Val Lys Ala Thr Val Asn Ala Ala Glu Ile Ser Gly

50

55

60

Glu Ala Arg Phe Val Val Pro Gly Asp Val Ile Gln Lys Met Val Lys

65

70

75

80

Val Leu Pro Asp Glu Ile Thr Glu Leu Ser Leu Glu Gly Asp Ala Leu

85

90

95

Val Ile Ser Ser Gly Ser Thr Val Phe Arg Ile Thr Thr Met Pro Ala
 100 105 110
 Asp Glu Phe Pro Glu Ile Thr Pro Ala Glu Ser Gly Ile Thr Phe Glu
 115 120 125
 Val Asp Thr Ser Leu Leu Glu Glu Met Val Glu Lys Val Ile Phe Ala
 130 135 140
 Ala Ala Lys Asp Glu Phe Met Arg Asn Leu Asn Gly Val Phe Trp Glu
 145 150 155 160
 Leu His Lys Asn Leu Leu Arg Leu Val Ala Ser Asp Gly Phe Arg Leu
 165 170 175
 Ala Leu Ala Glu Glu Gln Ile Glu Asn Glu Glu Glu Ala Ser Phe Leu
 180 185 190
 Leu Ser Leu Lys Ser Met Lys Glu Val Gln Asn Val Leu Asp Asn Thr
 195 200 205
 Thr Glu Pro Thr Ile Thr Val Arg Tyr Asp Gly Arg Arg Val Ser Leu
 210 215 220
 Ser Thr Asn Asp Val Glu Thr Val Met Arg Val Val Asp Ala Glu Phe
 225 230 235 240
 Pro Asp Tyr Lys Arg Val Ile Pro Glu Thr Phe Lys Thr Lys Val Val
 245 250 255
 Val Ser Arg Lys Glu Leu Arg Glu Ser Leu Lys Arg Val Met Val Ile
 260 265 270
 Ala Ser Lys Gly Ser Glu Ser Val Lys Phe Glu Ile Glu Glu Asn Val
 275 280 285
 Met Arg Leu Val Ser Lys Ser Pro Asp Tyr Gly Glu Val Val Asp Glu
 290 295 300
 Val Glu Val Gln Lys Glu Gly Glu Asp Leu Val Ile Ala Phe Asn Pro
 305 310 315 320
 Lys Phe Ile Glu Asp Val Leu Lys His Ile Glu Thr Glu Glu Ile Glu
 325 330 335
 Met Asn Phe Val Asp Ser Thr Ser Pro Cys Gln Ile Asn Pro Leu Asp
 340 345 350

Ile Ser Gly Tyr Leu Tyr Ile Val Met Pro Ile Arg Leu Ala
355 360 365

<210> 145
<211> 972
<212> DNA
<213> *Thermatoga maritima*

<400> 145
atgccagtca cgtttctcac aggtactgca gaaactcaga aggaagaatt gataaaagaaa 60
ctcctgaagg atggtaacgt ggagtacata aggatccatc cggaggatcc cgacaagatc 120
gatttcataa ggtctttact caggacaaag acgatcttt ccaacaagac gatcattgac 180
atcgtaatt tcgatgagtg gaaagcacag gagcagaagc gtctcggtga actttgaaa 240
aacgtaccgg aagacgttca tatcttcatc cgttctcaaa aaacagggtgg aaagggagta 300
gcgcgtggagc ttccgaagcc atgggaaacg gacaagtggc ttgagtgat agaaaagcgc 360
ttcagggaga atggtttgct catcgataaa gatgcccttc agctgtttt ctccaagggtt 420
ggaacgaacg acctgatcat agaaaagggag attgaaaaac tgaaaagctt ttccgaggac 480
agaaaagataa cggtagaaga cgtgaaagag gtcgttttta cctatcagac tccgggatac 540
gatgattttt gcttgctgt ttccgaagga aaaaggaagc tcgctcaactc tcttctgtcg 600
cagctgtgga aaaccacacaga gtccgtgggtt attgccactg tccttgcgaa tcacttctt 660
gatctcttca aaatcctcgt tcttgtgaca aagaaaaagat actacacctg gcctgatgtg 720
tccagggtgt ccaaagagct gggaaattccc gttcctcgtg tggctcggtt cctcggtttc 780
tccttaaga cctggaaattt caaggtgatg aaccacctcc tctactacga tgtgaagaag 840
gttagaaaga tactgaggga tctctacgat ctggacagag ccgtaaaaag cgaagaagat 900
ccaaaaccgt tcttccacga gttcatagaa gaggtggcac tggatgtata ttctcttcag 960
972
agagatgaag aa

<210> 146
<211> 324
<212> PRT
<213> *Thermatoga maritima*

<400> 146
Met Pro Val Thr Phe Leu Thr Gly Thr Ala Glu Thr Gln Lys Glu Glu
1 5 10 15
Leu Ile Lys Lys Leu Leu Lys Asp Gly Asn Val Glu Tyr Ile Arg Ile
20 25 30
His Pro Glu Asp Pro Asp Lys Ile Asp Phe Ile Arg Ser Leu Leu Arg
35 40 45
Thr Lys Thr Ile Phe Ser Asn Lys Thr Ile Ile Asp Ile Val Asn Phe
50 55 60

Asp	Glu	Trp	Lys	Ala	Gln	Glu	Gln	Lys	Arg	Leu	Val	Glu	Leu	Leu	Lys
65															80
				70										75	
Asn	Val	Pro	Glu	Asp	Val	His	Ile	Phe	Ile	Arg	Ser	Gln	Lys	Thr	Gly
															95
				85										90	
Gly	Lys	Gly	Val	Ala	Leu	Glu	Leu	Pro	Lys	Pro	Trp	Glu	Thr	Asp	Lys
															110
				100										105	
Trp	Leu	Glu	Trp	Ile	Glu	Lys	Arg	Phe	Arg	Glu	Asn	Gly	Leu	Leu	Ile
															125
				115										120	
Asp	Lys	Asp	Ala	Leu	Gln	Leu	Phe	Phe	Ser	Lys	Val	Gly	Thr	Asn	Asp
															140
				130										135	
Leu	Ile	Ile	Glu	Arg	Glu	Ile	Glu	Lys	Leu	Lys	Ala	Tyr	Ser	Glu	Asp
															160
				145										155	
Arg	Lys	Ile	Thr	Val	Glu	Asp	Val	Glu	Glu	Val	Val	Phe	Thr	Tyr	Gln
															175
				165										170	
Thr	Pro	Gly	Tyr	Asp	Asp	Phe	Cys	Phe	Ala	Val	Ser	Glu	Gly	Lys	Arg
															190
				180										185	
Lys	Leu	Ala	His	Ser	Leu	Leu	Ser	Gln	Leu	Trp	Lys	Thr	Thr	Glu	Ser
															205
				195										200	
Val	Val	Ile	Ala	Thr	Val	Leu	Ala	Asn	His	Phe	Leu	Asp	Leu	Phe	Lys
															220
				210										215	
Ile	Leu	Val	Leu	Val	Thr	Lys	Lys	Arg	Tyr	Tyr	Thr	Trp	Pro	Asp	Val
															240
				225										230	
Ser	Arg	Val	Ser	Lys	Glu	Leu	Gly	Ile	Pro	Val	Pro	Arg	Val	Ala	Arg
															255
				245										250	
Phe	Leu	Gly	Phe	Ser	Phe	Lys	Thr	Trp	Lys	Phe	Lys	Val	Met	Asn	His
															270
				260										265	
Leu	Leu	Tyr	Tyr	Asp	Val	Lys	Lys	Val	Arg	Lys	Ile	Leu	Arg	Asp	Leu
															285
				275										280	
Tyr	Asp	Leu	Asp	Arg	Ala	Val	Lys	Ser	Glu	Glu	Asp	Pro	Lys	Pro	Phe
															300
				290										295	
Phe	His	Glu	Phe	Ile	Glu	Glu	Val	Ala	Leu	Asp	Val	Tyr	Ser	Leu	Gln
															320
				305										310	
															315

Arg Asp Glu Glu

<210> 147
<211> 936
<212> DNA
<213> Thermatoga maritima

<400> 147
atgaacgatt tgatcagaaa gtacgctaaa gatcaactgg aaactttgaa aaggatcata 60
gaaaagtctg aaggaatatac catcctcata aatggagaag atctctcgta tccgagagaa 120
gtatcccttg aacttcccga gtacgtggag aaattcccc cgaaggcctc ggatgttctg 180
gagatagatc ccgaggggga gaacataggc atagacgaca tcagaacgat aaaggacttc 240
ctgaactaca gccccgagct ctacacgaga aagtacgtga tagtccacga ctgtgaaaga 300
atgacccagc aggcggcgaa cgcgttctg aaggccctg aagaaccacc agaatacgct 360
gtgatcggtc tgaacactcg ccgctggcat tatctactgc cgacgataaa gagccgagtg 420
ttcagagtgg ttgtgaacgt tccaaaggag ttcagagatc tcgtgaaaga gaaaatagga 480
gatctctggg aggaacttcc acttcttgag agagacttca aaacggctct cgaagcctac 540
aaacttggtg cgaaaaaaact ttctggattt atggaaagtc tcaaagttt ggagacggaa 600
aaactcttga aaaaggtcct ttcaaaaggc ctcgaagggtt atctcgcatg tagggagctc 660
ctggagagat ttcaaaaggt ggaatcgaag gaattcttg cgcttttga tcaggtgact 720
aacacgataa cagaaaaaga cgcgttctt ttgatccaga gactgacaag aatcattctc 780
cacaaaaaca catgggaaag cgttgaagat caaaaaagcg tgtcttcct cgattcaatt 840
ctcagggtga agatagcgaa tctgaacaac aaactcactc tcatgaacat cctcgcata 900
cacagagaga gaaagagagg tgtcaacgct tggagc 936

<210> 148
<211> 311
<212> PRT
<213> Thermatoga maritima

<400> 148
Met Asn Asp Leu Ile Arg Lys Tyr Ala Lys Asp Gln Leu Glu Thr Leu
1 5 10 15
Lys Arg Ile Ile Glu Lys Ser Glu Gly Ile Ser Ile Leu Ile Asn Gly
20 25 30
Glu Asp Leu Ser Tyr Pro Arg Glu Val Ser Leu Glu Leu Pro Glu Tyr
35 40 45
Val Glu Lys Phe Pro Pro Lys Ala Ser Asp Val Leu Glu Ile Asp Pro
50 55 60
Glu Gly Glu Asn Ile Gly Ile Asp Asp Ile Arg Thr Ile Lys Asp Phe
65 70 75 80

Leu Asn Tyr Ser Pro Glu Leu Tyr Thr Arg Lys Tyr Val Ile Val His
 85 90 95
 Asp Cys Glu Arg Met Thr Gln Gln Ala Ala Asn Ala Phe Leu Lys Ala
 100 105 110
 Leu Glu Glu Pro Pro Glu Tyr Ala Val Ile Val Leu Asn Thr Arg Arg
 115 120 125
 Trp His Tyr Leu Leu Pro Thr Ile Lys Ser Arg Val Phe Arg Val Val
 130 135 140
 Val Asn Val Pro Lys Glu Phe Arg Asp Leu Val Lys Glu Lys Ile Gly
 145 150 155 160
 Asp Leu Trp Glu Glu Leu Pro Leu Leu Glu Arg Asp Phe Lys Thr Ala
 165 170 175
 Leu Glu Ala Tyr Lys Leu Gly Ala Glu Lys Leu Ser Gly Leu Met Glu
 180 185 190
 Ser Leu Lys Val Leu Glu Thr Glu Lys Leu Leu Lys Lys Val Leu Ser
 195 200 205
 Lys Gly Leu Glu Gly Tyr Leu Ala Cys Arg Glu Leu Leu Glu Arg Phe
 210 215 220
 Ser Lys Val Glu Ser Lys Glu Phe Phe Ala Leu Phe Asp Gln Val Thr
 225 230 235 240
 Asn Thr Ile Thr Gly Lys Asp Ala Phe Leu Leu Ile Gln Arg Leu Thr
 245 250 255
 Arg Ile Ile Leu His Glu Asn Thr Trp Glu Ser Val Glu Asp Lys Ser
 260 265 270
 Val Ser Phe Leu Asp Ser Ile Leu Arg Val Lys Ile Ala Asn Leu Asn
 275 280 285
 Asn Lys Leu Thr Leu Met Asn Ile Leu Ala Ile His Arg Glu Arg Lys
 290 295 300
 Arg Gly Val Asn Ala Trp Ser
 305 310

<211> 423

<212> DNA

<213> Thermatoga maritima

<400> 149

atgtctttct tcaacaagat catactcata ggaagactcg tgagagatcc cgaagagaga 60
tacacgctca gcggaactcc agtcaccacc ttcaccatag cggtggacag ggttcccaga 120
aagaacgcgc cggacgacgc tcaaacgact gatttcttca ggatcgtcac ctttggaga 180
ctggcagagt tcgctagaac ctatctcacc aaaggaaggc tcgttctcggt cgaagggtgaa 240
atgagaatga gaagatggga aacacccact ggagaaaaaga gggtatctcc ggaggttgc 300
gcaaacgttg ttagattcat ggacagaaaa cctgctgaaa cagttagcga gactgaagag 360
gagctggaaa taccggaaga agactttcc agcgataacct tcagtgaaga tgaaccacca 420
423
ttt

<210> 150

<211> 141

<212> PRT

<213> Thermatoga maritima

<400> 150

Met Ser Phe Phe Asn Lys Ile Ile Leu Ile Gly Arg Leu Val Arg Asp
1 5 10 15

Pro Glu Glu Arg Tyr Thr Leu Ser Gly Thr Pro Val Thr Phe Thr
20 25 30

Ile Ala Val Asp Arg Val Pro Arg Lys Asn Ala Pro Asp Asp Ala Gln
35 40 45

Thr Thr Asp Phe Phe Arg Ile Val Thr Phe Gly Arg Leu Ala Glu Phe
50 55 60

Ala Arg Thr Tyr Leu Thr Lys Gly Arg Leu Val Leu Val Glu Gly Glu
65 70 75 80

Met Arg Met Arg Arg Trp Glu Thr Pro Thr Gly Glu Lys Arg Val Ser
85 90 95

Pro Glu Val Val Ala Asn Val Val Arg Phe Met Asp Arg Lys Pro Ala
100 105 110

Glu Thr Val Ser Glu Thr Glu Glu Leu Glu Ile Pro Glu Glu Asp
115 120 125

Phe Ser Ser Asp Thr Phe Ser Glu Asp Glu Pro Pro Phe
130 135 140

<210> 151
<211> 1353
<212> DNA
<213> Thermatoga maritima

<400> 151
atgcgtgttc cccgcacaa cttagaggcc gaagttgctg tgctcggaag catattgata 60
gatccgtcgg taataaacga cgttcttcaa atttttagcc acgaagattt ctatctgaaa 120
aaacaccaac acatcttcag akgatggaa gagcttacg acgaaggaaa accgggtggac 180
gtggtttccg tctgtgacaa gcttcaaagc atggaaaac tcgaggaat aggtggagat 240
ctgaaagtgg cccagctcgc tgaggctgtg cccagttctg cacacgcact tcactacgac 300
gagatcgtaa agaaaaatc cattctgagg aaactcattg agatctccag aaaaatctca 360
gaaagtgcct acatggaga agatgtggag atcctgctcg acaacgcaga aaagatgatc 420
ttcagatct cagagatgaa aacgacaaaaa tcctacgatc atctgagagg catcatgcac 480
cgggttttgg aaaaacctgga gaacttcagg gaaagagcca accttataga accgggtgtg 540
ctcataacgg gactaccaac gggattcaaa agtctggaca aacagaccac agggttccac 600
agctccgatc tgggataat agcagcgaga ccctccatgg gaaaaacctc cttcgactc 660
tcaatagcga ggaacatggc tgtcaatttc gaaatccccg tcggaatatt cagtctcgag 720
atgtccaagg aacagctcgc tcaaagacta ctcagcatgg agtccgggtg gatatcttac 780
agcatcagaa caggataacct ggatcaggag aagtggaaa gactcacaat agcggcttct 840
aaactctaca aagcacccat agttgtggac gatgagtac tcctcgatcc gcgatcggt 900
aggcggaaaag cgagaaggat gaaaaaaagaa tacgatgtaa aagccatttt tggactat 960
ctccagctca tgcacctgaa aggaagaaaa gaaagcagac agcaggagat atccgagatc 1020
tcgagatctc tgaagctcct tgcgagggaa ctcgacatag tggatagc gcttcacag 1080
cttcgaggg ccgtagaaca gagagaagac aaaagaccga ggctgagtgaa cctcaggaa 1140
tccggcgcga tagaacagga cgcagacaca gtcatctca tctacagggaa ggaatattac 1200
aggagcaaaa aatccaaaga gggaaagcaag cttcacgaac ctcacgaagc tgaaatcata 1260
ataggtaaac agagaaacgg tcccgttggaa acgatcactc tgatcttca ccccagaacg 1320
gttacgttcc atgaagtcga tgggtgcat tca 1353

<210> 152
<211> 451
<212> PRT
<213> Thermatoga maritima

<400> 152
Met Arg Val Pro Pro His Asn Leu Glu Ala Glu Val Ala Val Leu Gly
1 5 10 15

Ser Ile Leu Ile Asp Pro Ser Val Ile Asn Asp Val Leu Glu Ile Leu
20 25 30

Ser His Glu Asp Phe Tyr Leu Lys Lys His Gln His Ile Phe Arg Ala
35 40 45

Met Glu Glu Leu Tyr Asp Glu Gly Lys Pro Val Asp Val Val Ser Val

50	55	60
Cys Asp Lys Leu Gln Ser Met Gly Lys Leu Glu Glu Val Gly Gly Asp		
65	70	75
Leu Glu Val Ala Gln Leu Ala Glu Ala Val Pro Ser Ser Ala His Ala		
85	90	95
Leu His Tyr Ala Glu Ile Val Lys Glu Lys Ser Ile Leu Arg Lys Leu		
100	105	110
Ile Glu Ile Ser Arg Lys Ile Ser Glu Ser Ala Tyr Met Glu Glu Asp		
115	120	125
Val Glu Ile Leu Leu Asp Asn Ala Glu Lys Met Ile Phe Glu Ile Ser		
130	135	140
Glu Met Lys Thr Thr Lys Ser Tyr Asp His Leu Arg Gly Ile Met His		
145	150	155
Arg Val Phe Glu Asn Leu Glu Asn Phe Arg Glu Arg Ala Asn Leu Ile		
165	170	175
Glu Pro Gly Val Leu Ile Thr Gly Leu Pro Thr Gly Phe Lys Ser Leu		
180	185	190
Asp Lys Gln Thr Thr Gly Phe His Ser Ser Asp Leu Val Ile Ile Ala		
195	200	205
Ala Arg Pro Ser Met Gly Lys Thr Ser Phe Ala Leu Ser Ile Ala Arg		
210	215	220
Asn Met Ala Val Asn Phe Glu Ile Pro Val Gly Ile Phe Ser Leu Glu		
225	230	235
Met Ser Lys Glu Gln Leu Ala Gln Arg Leu Leu Ser Met Glu Ser Gly		
245	250	255
Val Asp Leu Tyr Ser Ile Arg Thr Gly Tyr Leu Asp Gln Glu Lys Trp		
260	265	270
Glu Arg Leu Thr Ile Ala Ala Ser Lys Leu Tyr Lys Ala Pro Ile Val		
275	280	285
Val Asp Asp Glu Ser Leu Leu Asp Pro Arg Ser Leu Arg Ala Lys Ala		
290	295	300
Arg Arg Met Lys Lys Glu Tyr Asp Val Lys Ala Ile Phe Val Asp Tyr		

305	310	315	320
Leu Gln Leu Met His Leu Lys Gly Arg Lys Glu Ser Arg Gln Gln Glu			
325	330	335	
Ile Ser Glu Ile Ser Arg Ser Leu Lys Leu Leu Ala Arg Glu Leu Asp			
340	345	350	
Ile Val Val Ile Ala Leu Ser Gln Leu Ser Arg Ala Val Glu Gln Arg			
355	360	365	
Glu Asp Lys Arg Pro Arg Leu Ser Asp Leu Arg Glu Ser Gly Ala Ile			
370	375	380	
Glu Gln Asp Ala Asp Thr Val Ile Phe Ile Tyr Arg Glu Glu Tyr Tyr			
385	390	395	400
Arg Ser Lys Lys Ser Lys Glu Glu Ser Lys Leu His Glu Pro His Glu			
405	410	415	
Ala Glu Ile Ile Ile Gly Lys Gln Arg Asn Gly Pro Val Gly Thr Ile			
420	425	430	
Thr Leu Ile Phe Asp Pro Arg Thr Val Thr Phe His Glu Val Asp Val			
435	440	445	
Val His Ser			
450			

<210> 153
<211> 1695
<212> DNA
<213> *Thermatoga maritima*

<400> 153

gtgattcctc gagaggtcat cgagggaaata aaagaaaaagg ttgacatcgt agaggtcatt 60
tccgagtacg tgaatcttac ccgggttaggt tcctcctaca gggctctctg tccctttcat 120
tcagaaacca atccttcttt ctacgttcat ccgggtttaa agatataccaa ttgtttcggc 180
tgcgggtcga gtggagacgt catcaaattt cttcaagaaaa tggaaaggat cagtttccag 240
gaagcgctgg aaagacttgc caaaagagct gggattgatc tttctctcta cagaacagaa 300
gggacttctg aatacggaaa atacattcgt ttgtacgaag aaacgtggaa aaggtaacgtc 360
aaagagctgg agaaatcgaa agaggcaaaa gactattaa aaagcagagg cttctctgaa 420
gaagatatacg caaagttcgg cttgggtac gtccccaaaga gatccagcat ctctatagaa 480
gttgcagaag gcatgaacat aacactggaa gaactgtca gatacggat cgcgctgaaa 540
aagggtgatc gattcgttga tagattcgaa ggaagaatcg ttgttccaaat aaagaacgac 600
agtggtcata ttgtggcttt tggtggcgt gctctcggca acgaagaacc gaagtatttg 660
aactctccag agaccaggtt aaaaaatcgaa aagaagaccc tttttctttt cgatgaggcg 720

aaaaaaagtgg caaaagaggt tggtttttc gtcatcaccg aaggctactt cgacgcgctc 780
gcattcagaa aggatgaat accaacggcg gtcgctgttc ttggggcgag tctttcaaga 840
gaggcgattc taaaacttgc ggcgtattcg aaaaacgtca tactgtgtt cgataatgac 900
aaagcaggct tcagagccac tctcaaattcc ctcgaggatc tcctagacta cgaattcaac 960
gtgcttgcgg caacccctc tccttacaaa gaccagatg aactcttca gaaagaagga 1020
gaaggttcat tgaaaaagat gctgaaaaac tcgcgttcgt tcgaatattt tctggtgacg 1080
gctggtgagg tcttcttgc caggaacagc cccgcgggtg tgagatccta ccttttttc 1140
ctcaaagggtt gggtccaaaa gatgagaagg aaaggatatt tgaaacacat agaaaatctc 1200
gtgaatgagg tttcatcttc tctccagata ccagaaaaacc agatttgaa ctttttgaa 1260
agcgacaggt ctaacactat gcctgttcat gagaccaagt cgtcaaaggt ttacgatgag 1320
gggagaggac tggcttattt gttttgaac tacgaggatt tgagggaaaa gattctggaa 1380
ctggacttag aggtactgga agataaaaaac gcgagggagt tttcaagag agtctcaactg 1440
ggagaagatt tgaacaaagt catagaaaaac ttcccaaaag agctgaaaga ctggattttt 1500
gagacaatag aaagcattcc tcctccaaag gatcccggaa aattcctcgg tgacctctcc 1560
gaaaagttga aaatccgacg gatagagaga cgtatcgcag aaatagatga tatgataaaag 1620
aaagcttcaa acgatgaaga aaggcgtctt cttctctcta tgaaagtggaa tctccctcaga 1680
aaaataaaga ggagg 1695

<210> 154

<211> 565

<212> PRT

<213> *Thermatoga maritima*

<400> 154

Met	Ile	Pro	Arg	Glu	Val	Ile	Glu	Glu	Ile	Lys	Glu	Lys	Val	Asp	Ile
1					5				10					15	

Val	Glu	Val	Ile	Ser	Glu	Tyr	Val	Asn	Leu	Thr	Arg	Val	Gly	Ser	Ser
								20				25		30	

Tyr	Arg	Ala	Leu	Cys	Pro	Phe	His	Ser	Glu	Thr	Asn	Pro	Ser	Phe	Tyr
								35				40		45	

Val	His	Pro	Gly	Leu	Lys	Ile	Tyr	His	Cys	Phe	Gly	Cys	Gly	Ala	Ser
					50				55			60			

Gly	Asp	Val	Ile	Lys	Phe	Leu	Gln	Glu	Met	Glu	Gly	Ile	Ser	Phe	Gln
						65			70		75		80		

Glu	Ala	Leu	Glu	Arg	Leu	Ala	Lys	Arg	Ala	Gly	Ile	Asp	Leu	Ser	Leu
							85			90			95		

Tyr	Arg	Thr	Glu	Gly	Thr	Ser	Glu	Tyr	Gly	Lys	Tyr	Ile	Arg	Leu	Tyr
								100			105		110		

Glu	Glu	Thr	Trp	Lys	Arg	Tyr	Val	Lys	Glu	Leu	Glu	Lys	Ser	Lys	Glu
								115		120		125			

Ala Lys Asp Tyr Leu Lys Ser Arg Gly Phe Ser Glu Glu Asp Ile Ala
 130 135 140
 Lys Phe Gly Phe Gly Tyr Val Pro Lys Arg Ser Ser Ile Ser Ile Glu
 145 150 155 160
 Val Ala Glu Gly Met Asn Ile Thr Leu Glu Glu Leu Val Arg Tyr Gly
 165 170 175
 Ile Ala Leu Lys Lys Gly Asp Arg Phe Val Asp Arg Phe Glu Gly Arg
 180 185 190
 Ile Val Val Pro Ile Lys Asn Asp Ser Gly His Ile Val Ala Phe Gly
 195 200 205
 Gly Arg Ala Leu Gly Asn Glu Glu Pro Lys Tyr Leu Asn Ser Pro Glu
 210 215 220
 Thr Arg Tyr Phe Ser Lys Lys Thr Leu Phe Leu Phe Asp Glu Ala
 225 230 235 240
 Lys Lys Val Ala Lys Glu Val Gly Phe Phe Val Ile Thr Glu Gly Tyr
 245 250 255
 Phe Asp Ala Leu Ala Phe Arg Lys Asp Gly Ile Pro Thr Ala Val Ala
 260 265 270
 Val Leu Gly Ala Ser Leu Ser Arg Glu Ala Ile Leu Lys Leu Ser Ala
 275 280 285
 Tyr Ser Lys Asn Val Ile Leu Cys Phe Asp Asn Asp Lys Ala Gly Phe
 290 295 300
 Arg Ala Thr Leu Lys Ser Leu Glu Asp Leu Leu Asp Tyr Glu Phe Asn
 305 310 315 320
 Val Leu Val Ala Thr Pro Ser Pro Tyr Lys Asp Pro Asp Glu Leu Phe
 325 330 335
 Gln Lys Glu Gly Glu Gly Ser Leu Lys Lys Met Leu Lys Asn Ser Arg
 340 345 350
 Ser Phe Glu Tyr Phe Leu Val Thr Ala Gly Glu Val Phe Phe Asp Arg
 355 360 365
 Asn Ser Pro Ala Gly Val Arg Ser Tyr Leu Ser Phe Leu Lys Gly Trp
 370 375 380

Val Gln Lys Met Arg Arg Lys Gly Tyr Leu Lys His Ile Glu Asn Leu
 385 390 395 400

Val Asn Glu Val Ser Ser Ser Leu Gln Ile Pro Glu Asn Gln Ile Leu
 405 410 415

Asn Phe Phe Glu Ser Asp Arg Ser Asn Thr Met Pro Val His Glu Thr
 420 425 430

Lys Ser Ser Lys Val Tyr Asp Glu Gly Arg Gly Leu Ala Tyr Leu Phe
 435 440 445

Leu Asn Tyr Glu Asp Leu Arg Glu Lys Ile Leu Glu Leu Asp Leu Glu
 450 455 460

Val Leu Glu Asp Lys Asn Ala Arg Glu Phe Phe Lys Arg Val Ser Leu
 465 470 475 480

Gly Glu Asp Leu Asn Lys Val Ile Glu Asn Phe Pro Lys Glu Leu Lys
 485 490 495

Asp Trp Ile Phe Glu Thr Ile Glu Ser Ile Pro Pro Pro Lys Asp Pro
 500 505 510

Glu Lys Phe Leu Gly Asp Leu Ser Glu Lys Leu Lys Ile Arg Arg Ile
 515 520 525

Glu Arg Arg Ile Ala Glu Ile Asp Asp Met Ile Lys Lys Ala Ser Asn
 530 535 540

Asp Glu Glu Arg Arg Leu Leu Leu Ser Met Lys Val Asp Leu Leu Arg
 545 550 555 560

Lys Ile Lys Arg Arg
 565

<210> 155
 <211> 804
 <212> DNA
 <213> *Thermus thermophilus*

<400> 155
 atggctctac acccggtca ccctggggca ataatcggtc acgaggccgt tctcgccctc 60
 ctccccggcc tcaccggcca gaccctgctc ttctccggcc ccgaggggggt gggcgccgc 120
 accgtggccc gctggtaacgc ctgggggctc aaccgcggct tccccccgccc 180
 gagcaccggg acgtcctcga ggtggggccc aaggcccggg acctccgggg ccggccgag 240

gtgcggctgg aggaggtggc gcccctttg gagtggtgct ccagccaccc ccgggagcgg 300
 gtgaaggtgg ccatccttga ctggcccac ctccttacccg aggccgcccgc caacccctc 360
 ctcaagctcc tggaggagcc cccttccatcg gcccgcacccg tcctcatcgcc cccaagccgc 420
 gccaccctcc tccccaccct ggctcccg gccacggagg tggcattcgcc ccccgtgccc 480
 gaggaggccc tgcgccctt caccaggac ccggagctcc tccgctacgc cgccggggcc 540
 ccggccgc tccttagggc cctccaggac ccggagggtt accgggcccgc catggccagg 600
 gcgaaaggc tcctgaaagc cccgcccctg gagcgcctcg ctttgcttcg ggagctttg 660
 gccgaggagg agggggtcca cgcctccac gccgtctaa agcgcggga gcacccctt 720
 gccctggagc gggcgccgggaa ggcctggag ggtaacgtga gccccgagct ggtcctcgcc 780
 cggtggct tagacttaga gaca 804

<210> 156

<211> 268

<212> PRT

<213> *Thermus thermophilus*

<400> 156

Met Ala Leu His Pro Ala His Pro Gly Ala Ile Ile Gly His Glu Ala
 1 5 10 15

Val Leu Ala Leu Leu Pro Arg Leu Thr Ala Gln Thr Leu Leu Phe Ser
 20 25 30

Gly Pro Glu Gly Val Gly Arg Arg Thr Val Ala Arg Trp Tyr Ala Trp
 35 40 45

Gly Leu Asn Arg Gly Phe Pro Pro Pro Ser Leu Gly Glu His Pro Asp
 50 55 60

Val Leu Glu Val Gly Pro Lys Ala Arg Asp Leu Arg Gly Arg Ala Glu
 65 70 75 80

Val Arg Leu Glu Glu Val Ala Pro Leu Leu Glu Trp Cys Ser Ser His
 85 90 95

Pro Arg Glu Arg Val Lys Val Ala Ile Leu Asp Ser Ala His Leu Leu
 100 105 110

Thr Glu Ala Ala Ala Asn Ala Leu Leu Lys Leu Leu Glu Glu Pro Pro
 115 120 125

Ser Tyr Ala Arg Ile Val Leu Ile Ala Pro Ser Arg Ala Thr Leu Leu
 130 135 140

Pro Thr Leu Ala Ser Arg Ala Thr Glu Val Ala Phe Ala Pro Val Pro
 145 150 155 160

Glu	Glu	Ala	Leu	Arg	Ala	Leu	Thr	Gln	Asp	Pro	Glu	Leu	Leu	Arg	Tyr
165														175	
Ala	Ala	Gly	Ala	Pro	Gly	Arg	Leu	Leu	Arg	Ala	Leu	Gln	Asp	Pro	Glu
180														190	
Gly	Tyr	Arg	Ala	Arg	Met	Ala	Arg	Ala	Gln	Arg	Val	Leu	Lys	Ala	Pro
195														205	
Pro	Leu	Glu	Arg	Leu	Ala	Leu	Leu	Arg	Glu	Leu	Leu	Ala	Glu	Glu	Glu
210														215	220
Gly	Val	His	Ala	Leu	His	Ala	Val	Leu	Lys	Arg	Pro	Glu	His	Leu	Leu
225														235	240
Ala	Leu	Glu	Arg	Ala	Arg	Glu	Ala	Leu	Glu	Gly	Tyr	Val	Ser	Pro	Glu
245														250	255
Leu	Val	Leu	Ala	Arg	Leu	Ala	Leu	Asp	Leu	Glu	Thr				
														260	265

<210> 157
 <211> 729
 <212> DNA
 <213> *Thermus thermophilus*

<400> 157
 atgctggacc tgagggaggt gggggaggcg gagtggaagg ccctaaagcc cctttggaa 60
 agcgtgccc agggcgcccc cgtcctccctc ctggacccta agccaagccc ctcccccggcg 120
 gccttctacc ggaaccggga aaggcgggac ttccccaccc ccaaggggaa ggacctggtg 180
 cggcacctgg aaaaccgggc caagcgcctg gggctcaggc tccccggcgg ggtggcccg 240
 tacctggct ccctggaggg ggacctcgag gcccctggagc gggagctgga gaagcttgc 300
 ctcctctccc caccctcac cctggagaag gtggagaagg tggtgccct gaggcccccc 360
 ctcacgggct ttgacctggt gcgctccgtc ctggagaagg accccaagga ggccctcctg 420
 cgccttaggcg gcctcaagga ggagggggag gagcccctca ggctcctcg ggccctctcc 480
 tggcagttcg ccctcctcgcc cggggccttc ttccctctcc gggaaaaccc caggcccaag 540
 gaggaggacc tcgcccgcct cgaggcccac ccctacgccc cccgcccgcg cctggaggcg 600
 gcgaaaggcgc tcacggaaga ggccctcaag gagggcctgg acggccctcat ggaggcggaa 660
 aagagggcca agggggggaa agacccgtgg ctcgcccctgg aggcggcggt cctccgcctc 720
 gcccgttga 729

<210> 158
 <211> 292
 <212> PRT
 <213> *Thermus thermophilus*

<400> 158

Met Val Ile Ala Phe Thr Gly Asp Pro Phe Leu Ala Arg Glu Ala Leu
1 5 10 15

Leu Glu Glu Ala Arg Leu Arg Gly Leu Ser Arg Phe Thr Glu Pro Thr
20 25 30

Pro Glu Ala Leu Ala Gln Ala Leu Ala Pro Gly Leu Phe Gly Gly Gly
35 40 45

Gly Ala Met Leu Asp Leu Arg Glu Val Gly Glu Ala Glu Trp Lys Ala
50 55 60

Leu Lys Pro Leu Leu Glu Ser Val Pro Glu Gly Val Pro Val Leu Leu
65 70 75 80

Leu Asp Pro Lys Pro Ser Pro Ser Arg Ala Ala Phe Tyr Arg Asn Arg
85 90 95

Glu Arg Arg Asp Phe Pro Thr Pro Lys Gly Lys Asp Leu Val Arg His
100 105 110

Leu Glu Asn Arg Ala Lys Arg Leu Gly Leu Arg Leu Pro Gly Gly Val
115 120 125

Ala Gln Tyr Leu Ala Ser Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg
130 135 140

Glu Leu Glu Lys Leu Ala Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys
145 150 155 160

Val Glu Lys Val Val Ala Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu
165 170 175

Val Arg Ser Val Leu Glu Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu
180 185 190

Gly Gly Leu Lys Glu Glu Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala
195 200 205

Leu Ser Trp Gln Phe Ala Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg
210 215 220

Glu Asn Pro Arg Pro Lys Glu Glu Asp Leu Ala Arg Leu Glu Ala His
225 230 235 240

Pro Tyr Ala Ala Arg Arg Ala Leu Glu Ala Ala Lys Arg Leu Thr Glu
245 250 255

Glu Ala Leu Lys Glu Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg
260 265 270

Ala Lys Gly Gly Lys Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu
275 280 285

Arg Leu Ala Arg
290

<210> 159
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 159 37
gtgtgtcata tgagtaagga tttcgtccac cttcacc

<210> 160
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 160 34
gtgtgtggat cggggacta ctcggaagta aggg

<210> 161
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 161 36
gtgtgtcata tggaaaccac aatattccag ttccag

<210> 162

<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 162
gtgtgtggat ccttatccac catgagaagt attttcac 39

<210> 163
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 163
gtgtgtcata tggaaaaagt ttttttggaa aaaaactcca g 41

<210> 164
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 164
gtgtgtggat ccttaatccg cctgaacggc taacg 35

<210> 165
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 165
gtgtgtcata tgaactacgt tcccttcgcg agaaagtaca g 41

<210> 166

<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 166
gtgtgtggat ccttaaaaca gcctcggtccc gctgga 36

<210> 167
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 167
gtgtgtcata tgcgcgtaa ggtggacagg gag 33

<210> 168
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 168
tgtgtctcga gtcatggcta caccctcatac ggcata 35

<210> 169
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 169
gtgtgtcata tgctcaataa gtttttataa ataggaagac ttacggg 47

<210> 170

<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 170
gtgtggatcc ttaaaaaggt atttcgtcct cttcatcgg 39

<210> 171
<211> 807
<212> DNA
<213> Thermus thermophilus

<400> 171
atggctcgag gcctgaaccg cgaaaaatcc atcgccgcgg tcgcccacccg gccggacatg 60
cgctacaccc cggcggggct cggcattttg gacctgaccc tcgcccgtca ggacctgctt 120
ctttccgata acggggggga accggaggtg tcctggtacc accgggtgag gctcttaggc 180
cgccaggcgg agatgtgggg cgacctcttg gaccaaggc agctcgctt cgtggagggc 240
cgccctggagt accgccaatgt gggaaaggaggg ggggagaagc ggagcgagct ccagatccgg 300
gccgacttcc ggaccccttg gacgaccggg ggaagaagcg ggcggaggac agccggggcc 360
agcccaggct cccgcggcc ctgaaccagg tcttcctcat gggcaacctg accccgggacc 420
cggaactccg ctacacccccc cagggcaccg cggtggcccg gctggccctg gcggtaacg 480
agcgccgcca gggggcggag gagcgcaccc acttcgtgga gttcaggcc tggcgccacc 540
tggcgagtg ggccgcggag ctgaggaagg gcgacggcct tttcgtgatc ggcagggtgg 600
tgaacgactc ctggaccagc tccagcggcg agcggcgctt ccagaccgt gtggaggccc 660
tcaggctgga gcgccccacc cgtggacctg cccaggcctg cccaggccgg cggAACAGGT 720
cccgcgaaat ccagacgggt ggggtggaca ttgacgaagg cttggaaagac tttccggccgg 780
aggaggattt gccgttttga gcacgaa 807

<210> 172
<211> 266
<212> PRT
<213> Thermus thermophilus

<400> 172
Met Ala Arg Gly Leu Asn Arg Val Phe Leu Ile Gly Ala Leu Ala Thr
1 5 10 15

Arg Pro Asp Met Arg Tyr Thr Pro Ala Gly Leu Ala Ile Leu Asp Leu
20 25 30

Thr Leu Ala Gly Gln Asp Leu Leu Leu Ser Asp Asn Gly Gly Glu Pro
35 40 45

Glu	Val	Ser	Trp	Tyr	His	Arg	Val	Arg	Leu	Leu	Gly	Arg	Gln	Ala	Glu
50							55					60			
Met	Trp	Gly	Asp	Leu	Leu	Asp	Gln	Gly	Gln	Leu	Val	Phe	Val	Glu	Gly
65							70				75			80	
Arg	Leu	Glu	Tyr	Arg	Gln	Trp	Glu	Arg	Glu	Gly	Glu	Lys	Arg	Ser	Glu
							85				90			95	
Leu	Gln	Ile	Arg	Ala	Asp	Phe	Leu	Asp	Pro	Leu	Asp	Asp	Arg	Gly	Lys
							100				105			110	
Lys	Arg	Ala	Glu	Asp	Ser	Arg	Gly	Gln	Pro	Arg	Leu	Arg	Ala	Ala	Leu
							115				120			125	
Asn	Gln	Val	Phe	Leu	Met	Gly	Asn	Leu	Thr	Arg	Asp	Pro	Glu	Leu	Arg
							130				135			140	
Tyr	Thr	Pro	Gln	Gly	Thr	Ala	Val	Ala	Arg	Leu	Gly	Leu	Ala	Val	Asn
							145				155			160	
Glu	Arg	Arg	Gln	Gly	Ala	Glu	Glu	Arg	Thr	His	Phe	Val	Glu	Val	Gln
							165				170			175	
Ala	Trp	Arg	Asp	Leu	Ala	Glu	Trp	Ala	Ala	Glu	Leu	Arg	Lys	Gly	Asp
							180				185			190	
Gly	Leu	Phe	Val	Ile	Gly	Arg	Leu	Val	Asn	Asp	Ser	Trp	Thr	Ser	Ser
							195				200			205	
Ser	Gly	Glu	Arg	Arg	Phe	Gln	Thr	Arg	Val	Glu	Ala	Leu	Arg	Leu	Glu
							210				215			220	
Arg	Pro	Thr	Arg	Gly	Pro	Ala	Gln	Ala	Cys	Pro	Gly	Arg	Arg	Asn	Arg
							225				230			235	
Ser	Arg	Glu	Val	Gln	Thr	Gly	Gly	Val	Asp	Ile	Asp	Glu	Gly	Leu	Glu
							245				250			255	
Asp	Phe	Pro	Pro	Glu	Glu	Asp	Leu	Pro	Phe						
							260				265				

<210> 173
 <211> 992
 <212> DNA
 <213> *Bacillus stearothermophilus*

<400> 173
aattccgaca tttcaattga atcgtttatt ccgcttgaaa aagaaggcaa gttgctcggt 60
gatgtgaaaa gaccggggag catcgtaactg caggcgcgc tttctctga aatcgtaaa 120
aaactgcccgc aacaaacggt ggaaatcgaa acggaagaca acttttgac gatcatccgc 180
tcggggcact cagaattccg cctcaatggg ctaaacgccc acgaatatcc gcgcctgccc 240
caaattgaag aagaaaacgt gttcaaatc ccggctgatt tattgaaaac cgtgattcgg 300
caaacggtgt tcgcccgttac tacatcgaa acgcgcacca tcttgacagg tgtcaactgg 360
aaagttgaac atggcgagct tgtctgcaca gcgaccgaca gtcatcgctt agccatgcgc 420
aaagtgaaaa ttgagtcgga aaatgaagta tcatacaacg tcgtcatccc tggaaaaagt 480
cttaatgagc tcagcaaaat tttggatgac ggcaaccacc cggtgacat cgtcatgaca 540
gccaatcaag tgctatttaa ggccgagcac cttcttct tttcccggt gcttgacggc 600
aactatccgg agacggcccg cttgattcca acagaaagca aaacgaccat gatcgtaat 660
gcaaaagagt ttctgcaggc aatcgaccga gcgtccttgc ttgctcgaga aggaaggaac 720
aacgttgtga aactgacgac gttcctgga ggaatgctcg aaatttcttc gatttctccg 780
agatcgggaa agtgaacggag cagctgcaaa cggagctct tgaaggggaa gagttgaaca 840
tttcgtttag cgcgaatataat atgatggacg cgttgcgggc gcttgatgga acagacattt 900
caaatcagct tcactgggc catgcggccg ttcctgttgc gcccgttca accgattcga 960
tgcttcagct cattttgccc gtgagaacat at 992

<210> 174
<211> 334
<212> PRT
<213> *Bacillus stearothermophilus*

<400> 174
Asn Ser Asp Ile Ser Ile Ile Glu Ser Phe Ile Pro Leu Glu Lys Glu
1 5 10 15
Gly Lys Leu Leu Val Asp Val Lys Arg Pro Gly Ser Ile Val Leu Gln
20 25 30
Ala Arg Phe Phe Ser Glu Ile Val Lys Lys Leu Pro Gln Gln Thr Val
35 40 45
Glu Ile Glu Thr Glu Asp Asn Phe Leu Thr Ile Ile Arg Ser Gly His
50 55 60
Ser Glu Phe Arg Leu Asn Gly Leu Asn Ala Asp Glu Tyr Pro Arg Leu
65 70 75 80
Pro Gln Ile Glu Glu Asn Val Phe Gln Ile Pro Ala Asp Leu Leu
85 90 95
Lys Thr Val Ile Arg Gln Thr Val Phe Ala Val Ser Thr Ser Glu Thr
100 105 110
Arg Pro Ile Leu Thr Gly Val Asn Trp Lys Val Glu His Gly Glu Leu

115	120	125	
Val Cys Thr Ala Thr Asp Ser His Arg Leu Ala Met Arg Lys Val Lys			
130	135	140	
Ile Ile Glu Ser Glu Asn Glu Val Ser Tyr Asn Val Val Ile Pro Gly			
145	150	155	160
Lys Ser Leu Asn Glu Leu Ser Lys Ile Ile Leu Asp Asp Gly Asn His			
165	170	175	
Pro Val Asp Ile Val Met Thr Ala Asn Gln Val Leu Phe Lys Ala Glu			
180	185	190	
His Leu Leu Phe Phe Ser Arg Leu Leu Asp Gly Asn Tyr Pro Glu Thr			
195	200	205	
Ala Arg Leu Ile Pro Thr Glu Ser Lys Thr Thr Met Ile Val Asn Ala			
210	215	220	
Lys Glu Phe Leu Gln Ala Ile Asp Arg Ala Ser Leu Leu Ala Arg Glu			
225	230	235	240
Gly Arg Asn Asn Val Val Lys Leu Thr Thr Leu Pro Gly Gly Met Leu			
245	250	255	
Glu Ile Ser Ser Ile Ser Pro Glu Ile Gly Lys Val Thr Glu Gln Leu			
260	265	270	
Gln Thr Glu Ser Leu Glu Gly Glu Glu Leu Asn Ile Ser Phe Ser Ala			
275	280	285	
Lys Tyr Met Met Asp Ala Leu Arg Ala Leu Asp Gly Thr Asp Ile Gln			
290	295	300	
Ile Ser Phe Thr Gly Ala Met Arg Pro Phe Leu Leu Arg Pro Leu His			
305	310	315	320
Thr Asp Ser Met Leu Gln Leu Ile Leu Pro Val Arg Thr Tyr			
325	330		

<210> 175
 <211> 492
 <212> DNA
 <213> *Bacillus stearothermophilus*

 <400> 175

atgattaacc gcgtcatttt ggtcggcagg ttaacgagag atccggagtt gcgttacact 60
ccaagcgag tggctgttgc cacgttacg ctcgcggtca accgtccgtt tacaatcag 120
cagggcgagc gggaaacgga ttttattcaa tgtgtcggtt ggcgcgcaca ggcggaaaac 180
gtcgccaact ttttgaaaaa ggggagctt gctgggtcg atggccgact gcaaaccgc 240
agctatgaaa atcaagaagg tcggcgtgt tacgtacgg aagtggtgc tgatagcg 300
caatttctt agccgaaagg aacgagcgag cagcgggggg cgacagcagg cggtactat 360
gggatccat tcccatcg gcaagatcg aaccaccaat atccgaacga aaaagggtt 420
ggccgcatcg atgacgatcc ttgcgcatt gacggccagc cgatcgatat ttctgatgtat 480
gatttgcgt tt 492

<210> 176

<211> 164

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 176

Met Ile Asn Arg Val Ile Leu Val Gly Arg Leu Thr Arg Asp Pro Glu
1 5 10 15

Leu Arg Tyr Thr Pro Ser Gly Val Ala Val Ala Thr Phe Thr Leu Ala
20 25 30

Val Asn Arg Pro Phe Thr Asn Gln Ser Tyr Glu Asn Gln Glu Gly Arg
35 40 45

Arg Val Tyr Val Thr Glu Val Val Ala Asp Ser Val Gln Phe Leu Glu
50 55 60

Pro Lys Gly Thr Ser Glu Gln Arg Gly Ala Thr Ala Gly Gly Tyr Tyr
65 70 75 80

Gln Gly Glu Arg Glu Thr Asp Phe Ile Gln Cys Val Val Trp Arg Arg
85 90 95

Gln Ala Glu Asn Val Ala Asn Phe Leu Lys Lys Gly Ser Leu Ala Gly
100 105 110

Val Asp Gly Arg Leu Gln Thr Arg Gly Asp Pro Phe Pro Phe Gly Gln
115 120 125

Asp Gln Asn His Gln Tyr Pro Asn Glu Lys Gly Phe Gly Arg Ile Asp
130 135 140

Asp Asp Pro Phe Ala Asn Asp Gly Gln Pro Ile Asp Ile Ser Asp Asp
145 150 155 160

Asp Leu Pro Phe

<210> 177
<211> 1044
<212> DNA
<213> *Bacillus stearothermophilus*

<400> 177
atgctggAAC gcgtatgggg aaacattgaa aaacggcgTT tttctccCT ttatttatta 60
tacggcaatg agccgtttt attaacggaa acgtatgagc gattggtaa cgcaGcgCTT 120
ggccccgagg agcgggagtG gaacttggct gtgtacgact gcgagGAAC gccgatcgag 180
gcggcgcttG aggaggcga gacggtgccG ttttcggcg agcggcgTGT cattctcatc 240
aagcatccat attttttac gtctgaaaaa gagaaggaga tcgaacatga tttggcgaag 300
ctggaggcgT acttgaaggc gccgtcgccG tttcgatcg tcgtctttt cgcggccgtac 360
gagaagcttG atgagcgaaa aaaaattacg aagctcgccA aagagcaaaAG cgaagtcgtc 420
atcgccgccc cgctcgccG agcggagctG cgtgcctggG tgccggccG catcgagAGc 480
caaggggcgc aagcaagcga cgaggcgatt gatgtcctgt tgccggggc cgggacgcag 540
cttccgcct tggcgaatga aatcgataaa ttggccctgt ttgcccgtc gggcggacc 600
atcgaggcgg cggcggttga gccgcttgc gcccgcacgc cggaaagaaaa cgtatttgc 660
cttgcgagc aagtggcgaa gccgcgacatt ccagcagcgt tgccgacgtt ttatgatctg 720
cttgaaaaaca atgaagagcc gatcaaaaatt ttggcggttgc tgccgcctca tttccgcctg 780
cttgcgcaag tgaatggct tgccctccta ggctacggac aggcgcaaaAT tgctgcggcg 840
ctcaagggtgc acccggttccG cgtcaagctc gctcttgctc aagcggcccg cttcgctgac 900
ggagagcttG ctgaggcgat caacgagctc gctgacgcccG attacgaagt gaaaagcggg 960
gcgggtcgatc gccggttggc cgttgagctG cttctgatgc gctggggcgc cggccggcg 1020
caagcggggc gccacggccG gccc 1044

<210> 178
<211> 348
<212> PRT
<213> *Bacillus stearothermophilus*

<400> 178
Met Leu Glu Arg Val Trp Gly Asn Ile Glu Lys Arg Arg Phe Ser Pro
1 5 10 15

Leu Tyr Leu Leu Tyr Gly Asn Glu Pro Phe Leu Leu Thr Glu Thr Tyr
20 25 30

Glu Arg Leu Val Asn Ala Ala Leu Gly Pro Glu Glu Arg Glu Trp Asn
35 40 45

Leu Ala Val Tyr Asp Cys Glu Glu Thr Pro Ile Glu Ala Ala Leu Glu
50 55 60

Glu Ala Glu Thr Val Pro Phe Phe Gly Glu Arg Arg Val Ile Leu Ile

65	70	75	80
Lys His Pro Tyr Phe Phe Thr Ser Glu Lys Glu Lys Glu Ile Glu His			
85	90	95	
Asp Leu Ala Lys Leu Glu Ala Tyr Leu Lys Ala Pro Ser Pro Phe Ser			
100	105	110	
Ile Val Val Phe Phe Ala Pro Tyr Glu Lys Leu Asp Glu Arg Lys Lys			
115	120	125	
Ile Thr Lys Leu Ala Lys Glu Gln Ser Glu Val Val Ile Ala Ala Pro			
130	135	140	
Leu Ala Glu Ala Glu Leu Arg Ala Trp Val Arg Arg Arg Ile Glu Ser			
145	150	155	160
Gln Gly Ala Gln Ala Ser Asp Glu Ala Ile Asp Val Leu Leu Arg Arg			
165	170	175	
Ala Gly Thr Gln Leu Ser Ala Leu Ala Asn Glu Ile Asp Lys Leu Ala			
180	185	190	
Leu Phe Ala Gly Ser Gly Gly Thr Ile Glu Ala Ala Ala Val Glu Arg			
195	200	205	
Leu Val Ala Arg Thr Pro Glu Glu Asn Val Phe Val Leu Val Glu Gln			
210	215	220	
Val Ala Lys Arg Asp Ile Pro Ala Ala Leu Gln Thr Phe Tyr Asp Leu			
225	230	235	240
Leu Glu Asn Asn Glu Glu Pro Ile Lys Ile Leu Ala Leu Leu Ala Ala			
245	250	255	
His Phe Arg Leu Leu Ser Gln Val Lys Trp Leu Ala Ser Leu Gly Tyr			
260	265	270	
Gly Gln Ala Gln Ile Ala Ala Leu Lys Val His Pro Phe Arg Val			
275	280	285	
Lys Leu Ala Leu Ala Gln Ala Ala Arg Phe Ala Asp Gly Glu Leu Ala			
290	295	300	
Glu Ala Ile Asn Glu Leu Ala Asp Ala Asp Tyr Glu Val Lys Ser Gly			
305	310	315	320
Ala Val Asp Arg Arg Leu Ala Val Glu Leu Leu Leu Met Arg Trp Gly			

325

330

335

Ala Arg Pro Ala Gln Ala Gly Arg His Gly Arg Arg
340 345

<210> 179
<211> 757
<212> DNA
<213> *Bacillus stearothermophilus*

<400> 179
atgcgatggg aacagctagc gaaacgccag ccgggtggc cgaaaatgct gcaaagcgcc 60
ttggaaaaag ggcggatttc tcatgcgtac ttgtttgagg ggcagcgggg gacgggcaaa 120
aaagcggcca gtttgtgtt ggcgaaacgt ttgtttgtc tgtccccat cgaggtttcc 180
ccgtgtctag agtgcgc aa ctgcccgc atcgactccg gcaaccaccc tgacgtccgg 240
gtgatcgcc cagatggagg atcaatcaa aaggaacaaa tcgaatggct gcagcaagag 300
ttctcgaaaa cagcggtcga gtcggataaa aaaatgtaca tcgttgagca cgccgatcaa 360
atgacgacaa ggcgtccaa cagccttctg aaattttgg aagagccgca tccggggacg 420
gtggcgttat tgctgactga gcaataccac cgccctgctag ggacgatcgt ttcccgctgt 480
caagtgc tt cgtccggcc gttgccgccc gcagagctcg cccagggact tgtcgaggag 540
cacgtgccgt tgccgttggc gctgttggc gcccatttga caaacagctt cgaggaagca 600
ctggcgcttg ccaaagatag ttgggttgc gaggcgccaa cattagtgt acaatggat 660
gagatgctgg gcaagccgga gctgcagctt ttgttttca tccacgaccg cttgttccg 720
catttttgg aaagccatca gcttgacctt ggacttg 757

<210> 180
<211> 252
<212> PRT
<213> *Bacillus stearothermophilus*

<400> 180
Met Arg Trp Glu Gln Leu Ala Lys Arg Gln Pro Val Val Ala Lys Met
1 5 10 15

Leu Gln Ser Gly Leu Glu Lys Gly Arg Ile Ser His Ala Tyr Leu Phe
20 25 30

Glu Gly Gln Arg Gly Thr Gly Lys Lys Ala Ala Ser Leu Leu Leu Ala
35 40 45

Lys Arg Leu Phe Cys Leu Ser Pro Ile Gly Val Ser Pro Cys Leu Glu
50 55 60

Cys Arg Asn Cys Arg Arg Ile Asp Ser Gly Asn His Pro Asp Val Arg
65 70 75 80

Val	Ile	Gly	Pro	Asp	Gly	Gly	Ser	Ile	Lys	Lys	Glu	Gln	Ile	Glu	Trp
														95	
Leu	Gln	Gln	Glu	Phe	Ser	Lys	Thr	Ala	Val	Glu	Ser	Asp	Lys	Lys	Met
														110	
Tyr	Ile	Val	Glu	His	Ala	Asp	Gln	Met	Thr	Thr	Ser	Ala	Ala	Asn	Ser
														125	
Leu	Leu	Lys	Phe	Leu	Glu	Glu	Pro	His	Pro	Gly	Thr	Val	Ala	Val	Leu
														140	
Leu	Thr	Glu	Gln	Tyr	His	Arg	Leu	Leu	Gly	Thr	Ile	Val	Ser	Arg	Cys
														160	
145															
Gln	Val	Leu	Ser	Phe	Arg	Pro	Leu	Pro	Pro	Ala	Glu	Leu	Ala	Gln	Gly
														175	
Leu	Val	Glu	Glu	His	Val	Pro	Leu	Pro	Leu	Ala	Leu	Leu	Ala	Ala	His
														190	
180															
Leu	Thr	Asn	Ser	Phe	Glu	Glu	Ala	Leu	Ala	Leu	Ala	Lys	Asp	Ser	Trp
														205	
Phe	Ala	Glu	Ala	Arg	Thr	Leu	Val	Leu	Gln	Trp	Tyr	Glu	Met	Leu	Gly
														220	
210															
Lys	Pro	Glu	Leu	Gln	Leu	Leu	Phe	Phe	Ile	His	Asp	Arg	Leu	Phe	Pro
														240	
225															
His	Phe	Leu	Glu	Ser	His	Gln	Leu	Asp	Leu	Gly	Leu				
														250	

<210> 181

<211> 1677

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 181

gtggcatacc aagcgttata tcgcgtgtt cggccgcagc gctttgcgga catggtcggc 60
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 tacttatttt ccggcccgcg cggtacagga aaaacgagcg cagcggaaaat tttcgccaag 180
 gcggtaact gtgaacaggc gccagcggcg gagccatgca atgagtgtcc agcttgcctc 240
 ggcattacga atgaaacggt tcccgtatgt ctggaaattt acgctgttttcaacaaccgc 300
 gtcgtatgaaatccgtgatat ccgtgagaag gtgaaatttgc gccaacgtc ggcccgctac 360
 aaaatgttata tcatcgacga ggtgcataatgc ctgtcgatgc gtgcgtttaa cgcgtgttg 420
 aaaacgttgg aggagccgcc gaaacacgac attttcattt tggccacgac cgagccgcac 480

aaaattccgg cgacgatcat ttcccgtgc caacggttcg attttcgccc catcccgctt 540
caggcgatcg tttcacggct aaagtacgtc gcaagcgccc aagggtgtcg ggcgtcagat 600
gaggcattgt ccgcacatcgcc cctgtgtcga gacggggggta tgcgcgtatgc gctcagctt 660
cttgcgtcaag ccatttcgtt cagcgacggg aaacttcggc tcgacgacgt gctggcgatg 720
accggggctg catcattgc cgccttatacg agcttcatcg aagccatcca cgcacaagat 780
acagcggcgg ttcttcagca cttggaaacg atgatggcgc aaggggaaaga tccgcacatcg 840
ttgggttgaag acttgatttt gtactatcgc gatttattgc tgtacaaaac cgctccctat 900
gtggaggggag cgattcaaataat tgctgtcgtt gacgaagcgt tcacttcact gtcggaaatg 960
attccggttt ccaatttata cgaggccatc gagttgtcg acaaaaagcca gcaagagatg 1020
aagtggacaa accaccccgcc cttctgtt gaaatggcgc ttgtgaaact ttgcacatcca 1080
tcagccgccc ccccggtcgct gtcggcttcc gagttggAAC cggtgataaa gcggattgaa 1140
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gcccgggtga aaaaactgtc caaaccgtatg aaaacggggg gatataaaagc cccgggttggc 1260
cgcatttacg agctgttgcgaa acaggcgacg catgaagatt tagcttttgtt gaaaggatgc 1320
tggggcgatgt tgctcgacac gttgaaacgg cagcataaaag tgcgcacgc tgccttgctg 1380
caagagagcg agccgggtgc agcgagcgcc tcagcgttt gatataaaatt caaatacgaa 1440
atccactgca aaatggcgac cgatcccaca agttcggtca aagaaaacgt cgaagcgatt 1500
ttgtttgagc tgacaaaaccg ccgctttgaa atggtagcca ttccggaggg agaatgggg 1560
aaaataagag aagagttcat ccgcaataaag gacggcatgg tggaaaaaaag cgaagaagat 1620
ccgttaatcg ccgaagcgaa gcggctgtt ggcgaagagc tgatcgaaat taaagaa 1677

<210> 182

<211> 559

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 182

Val	Ala	Tyr	Gln	Ala	Leu	Tyr	Arg	Val	Phe	Arg	Pro	Gln	Arg	Phe	Ala
1								10						15	

Asp	Met	Val	Gly	Gln	Glu	His	Val	Thr	Lys	Thr	Leu	Gln	Ser	Ala	Leu
		20						25						30	

Leu	Gln	His	Lys	Ile	Ser	His	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly
		35				40						45			

Thr	Gly	Lys	Thr	Ser	Ala	Ala	Lys	Ile	Phe	Ala	Lys	Ala	Val	Asn	Cys
		50				55					60				

Glu	Gln	Ala	Pro	Ala	Ala	Glu	Pro	Cys	Asn	Glu	Cys	Pro	Ala	Cys	Leu
		65				70			75			80			

Gly	Ile	Thr	Asn	Gly	Thr	Val	Pro	Asp	Val	Leu	Glu	Ile	Asp	Ala	Ala
		85				90					95				

Ser	Asn	Asn	Arg	Val	Asp	Glu	Ile	Arg	Asp	Ile	Arg	Glu	Lys	Val	Lys
		100				105					110				

Phe Ala Pro Thr Ser Ala Arg Tyr Lys Val Tyr Ile Ile Asp Glu Val
115 120 125

His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Lys His Val Ile Phe Ile Leu Ala Thr Thr Glu Pro His
145 150 155 160

Lys Ile Pro Ala Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Arg
165 170 175

Arg Ile Pro Leu Gln Ala Ile Val Ser Arg Leu Lys Tyr Val Ala Ser
180 185 190

Ala Gln Gly Val Glu Ala Ser Asp Glu Ala Leu Ser Ala Ile Ala Arg
195 200 205

Ala Ala Asp Gly Gly Met Arg Asp Ala Leu Ser Leu Leu Asp Gln Ala
210 215 220

Ile Ser Phe Ser Asp Gly Lys Leu Arg Leu Asp Asp Val Leu Ala Met
225 230 235 240

Thr Gly Ala Ala Ser Phe Ala Ala Leu Ser Ser Phe Ile Glu Ala Ile
245 250 255

His Arg Lys Asp Thr Ala Ala Val Leu Gln His Leu Glu Thr Met Met
260 265 270

Ala Gln Gly Lys Asp Pro His Arg Leu Val Glu Asp Leu Ile Leu Tyr
275 280 285

Tyr Arg Asp Leu Leu Tyr Lys Thr Ala Pro Tyr Val Glu Gly Ala
290 295 300

Ile Gln Ile Ala Val Val Asp Glu Ala Phe Thr Ser Leu Ser Glu Met
305 310 315 320

Ile Pro Val Ser Asn Leu Tyr Glu Ala Ile Glu Leu Leu Asn Lys Ser
325 330 335

Gln Gln Glu Met Lys Trp Thr Asn His Pro Arg Leu Leu Leu Glu Val
340 345 350

Ala Leu Val Lys Leu Cys His Pro Ser Ala Ala Ala Pro Ser Leu Ser
355 360 365

150

Ala Ser Glu Leu Glu Pro Leu Ile Lys Arg Ile Glu Thr Leu Glu Ala
 370 375 380

 Glu Leu Arg Arg Leu Lys Glu Gln Pro Pro Ala Pro Pro Ser Thr Ala
 385 390 395 400

 Ala Pro Val Lys Lys Leu Ser Lys Pro Met Lys Thr Gly Gly Tyr Lys
 405 410 415

 Ala Pro Val Gly Arg Ile Tyr Glu Leu Leu Lys Gln Ala Thr His Glu
 420 425 430

 Asp Leu Ala Leu Val Lys Gly Cys Trp Ala Asp Val Leu Asp Thr Leu
 435 440 445

 Lys Arg Gln His Lys Val Ser His Ala Ala Leu Leu Gln Glu Ser Glu
 450 455 460

 Pro Val Ala Ala Ser Ala Ser Ala Phe Val Leu Lys Phe Lys Tyr Glu
 465 470 475 480

 Ile His Cys Lys Met Ala Thr Asp Pro Thr Ser Ser Val Lys Glu Asn
 485 490 495

 Val Glu Ala Ile Leu Phe Glu Leu Thr Asn Arg Arg Phe Glu Met Val
 500 505 510

 Ala Ile Pro Glu Gly Glu Trp Gly Lys Ile Arg Glu Glu Phe Ile Arg
 515 520 525

 Asn Lys Asp Ala Met Val Glu Lys Ser Glu Glu Asp Pro Leu Ile Ala
 530 535 540

 Glu Ala Lys Arg Leu Phe Gly Glu Glu Leu Ile Glu Ile Lys Glu
 545 550 555

<210> 183
 <211> 4301
 <212> DNA
 <213> *Bacillus stearothermophilus*

<400> 183
 atggtgacaa aagagcaaaa agagcggttt ctcatcctgc ttgagcagct gaagatgacg 60
 tcgacgaaat ggatgccgca ttttcgttag gcagccattc gcaaagtctgt gatcgataaa 120
 gagagaaaaa gctggcattt ttatttcag ttcgacaacg tgctgccggt tcatgtatac 180
 aaaacgtttc ccgatcggtt gcagacggcg ttccggccata tcggccggcgt ccggccatacg 240

atggaggtcg aagcgccg 300
cttgcgcgc tgcaagaagg 360
gagctgaaag 420
aaacggcggt 480
cagcttgacg 540
cagaagagg 600
aaggccg 660
gagccggtgc 720
tatgtat 780
atcacagatt 840
gagcttatga 900
gatacg 960
gaacggcaag 1020
atgagccaaa 1080
ggcattccgg 1140
agcgcggcga 1200
gatggcgtgc 1260
gtctttgacg 1320
gcggtaaag 1380
catccgttgc 1440
gttgc 1500
gttgc 1560
gttgc 1620
gattgaaaa 1680
catcaccgcg 1740
gaagcggaag 1800
gcttc 1860
ttgaaaaatt 1920
cgcatcccgc 1980
gacaaaggag 2040
gcccgtttt 2100
atggattatg 2160
ggtgagaagc 2220
gataaaaattt 2280
catgaactgc 2340
tttagggccgg 2400
atcggcgatg 2460
gaggaaatca 2520
aaacttgg 2580
gtcatttatt 2640
gggtcg 2700
aatccgctgc 2760
ggttc 2820
tacaagaaag 2880
gtgccggata 2940
aaagtgc 3000
aaaacggcg 3060
gcggaaatcg 3120

cgggcgccat catcgctgatccggattata tggaaatccaat 3180
atccggccga tgacacgtcc tctgaatggc ggacgaccca tttcgacttc cattcgatcc 3240
acgacaattt gtgaaagctc gatattctcg ggcacgacga tccgacggtc attcgatgc 3300
tgcaagattt aagcgccatc gatccgaaaa cgatccgac cgacgacccg gatgtatgg 3360
gcattttcag cagcaccggag ccgcttggcg ttacgcccga gcaaatcatg tgcaatgtcg 3420
gcacgatcgg cattccggag ttggcacgc gcttcgttcg gcaaatgttg gaagagacaa 3480
ggccaaaaac gtttccgaa ctcgtcaaa ttccggctt gtcgcacggc accgatgtgt 3540
ggctcgccaa cgcgcaagag ctcattcaaa acggcacgtg tacgttatcg gaagtcatcg 3600
gctgcccgaa cgacattatg gtctatttga ttaccggcg gctcgagccg tcgctcgctt 3660
ttaaaatcat ggaatccgtg cgcaaaaggaa aaggcttaac gcccggagttt gaagcagaaaa 3720
tgcgcaaaaca tgacgtgccc gagtggtaca tcgattcatg caaaaaaaatc aagtacatgt 3780
tcccggaaagc gcacgcccgc gcctacgtgt taatggccgt ggcacatcgcc tactttaagg 3840
tgcaccatcc gctttgtat tacgctgtcgt actttacggt gccccggag gactttgacc 3900
ttgacgccccat gatcaaaggaa tcacccgcca ttgcacggcg gattgaggaa atcaacgcca 3960
aaggcattca ggcgcacggcg aaagaaaaaaa gcttgctcac ggttcttgag gtggcccttag 4020
agatgtgcga ggcgcggctt tcctttaaaa atatcgattt gtaccgctcg caggcgacgg 4080
aattcgatcat tgacggcaat tctctcattc cgccgttcaa cgccattccg gggcttggga 4140
cgaacgtggc gcaggcgatc gtgcgcgccc gcgaggaagg cgagtttttgcgatctcg 4200
atttgcacaaca ggcggccaaa ttgtcgaaaa cgctgctcgatctcgatctcg 4260
gccttgcgttgcgttcccgacataaccagc tgtcgttgcgtt t 4301

<210> 184

<211> 1433

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 184

Met	Val	Thr	Lys	Glu	Gln	Lys	Glu	Arg	Phe	Leu	Ile	Leu	Leu	Glu	Gln
1				5					10					15	

Leu Lys Met Thr Ser Asp Glu Trp Met Pro His Phe Arg Glu Ala Ala
20 25 30

Ile	Arg	Lys	Val	Val	Ile	Asp	Lys	Glu	Glu	Lys	Ser	Trp	His	Phe	Tyr
35							40						45		

Phe Gln Phe Asp Asn Val Leu Pro Val His Val Tyr Lys Thr Phe Ala
50 55 60

Asp Arg Leu Gln Thr Ala Phe Arg His Ile Ala Ala Val Arg His Thr
65 . 70 75 80

Met Glu Val Glu Ala Pro Arg Val Thr Glu Ala Asp Val Gln Ala Tyr
85 90 95

Trp Pro Leu Cys Leu Ala Glu Leu Gln Glu Gly Met Ser Pro Leu Val
 100 105 110

Asp Trp Leu Ser Arg Gln Thr Pro Glu Leu Lys Gly Asn Lys Leu Leu
 115 120 125
 Val Val Ala Arg His Glu Ala Glu Ala Leu Ala Ile Lys Arg Arg Phe
 130 135 140
 Ala Lys Lys Ile Ala Asp Val Tyr Ala Ser Phe Gly Phe Pro Pro Leu
 145 150 155 160
 Gln Leu Asp Val Ser Val Glu Pro Ser Lys Gln Glu Met Glu Gln Phe
 165 170 175
 Leu Ala Gln Lys Gln Gln Glu Asp Glu Glu Arg Ala Leu Ala Val Leu
 180 185 190
 Thr Asp Leu Ala Arg Glu Glu Lys Ala Ala Ser Ala Pro Pro Ser
 195 200 205
 Gly Pro Leu Val Ile Gly Tyr Pro Ile Arg Asp Glu Glu Pro Val Arg
 210 215 220
 Arg Leu Glu Thr Ile Val Glu Glu Arg Arg Val Val Val Gln Gly
 225 230 235 240
 Tyr Val Phe Asp Ala Glu Val Ser Glu Leu Lys Ser Gly Arg Thr Leu
 245 250 255
 Leu Thr Met Lys Ile Thr Asp Tyr Thr Asn Ser Ile Leu Val Lys Met
 260 265 270
 Phe Ser Arg Asp Lys Glu Asp Ala Glu Leu Met Ser Gly Val Lys Lys
 275 280 285
 Gly Met Trp Val Lys Val Arg Gly Ser Val Gln Asn Asp Thr Phe Val
 290 295 300
 Arg Asp Leu Val Ile Ile Ala Asn Asp Leu Asn Glu Ile Ala Ala Asn
 305 310 315 320
 Glu Arg Gln Asp Thr Ala Pro Glu Gly Glu Lys Arg Val Glu Leu His
 325 330 335
 Leu His Thr Pro Met Ser Gln Met Asp Ala Val Thr Ser Val Thr Lys
 340 345 350
 Leu Ile Glu Gln Ala Lys Lys Trp Gly His Pro Ala Ile Ala Val Thr
 355 360 365

Asp His Ala Val Val Gln Ser Phe Pro Glu Ala Tyr Ser Ala Ala Lys
370 375 380

Lys His Gly Met Lys Val Ile Tyr Gly Leu Glu Ala Asn Ile Val Asp
385 390 395 400

Asp Gly Val Pro Ile Ala Tyr Asn Glu Thr His Arg Arg Leu Ser Glu
405 410 415

Glu Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val
420 425 430

Tyr Asn Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Asp Gly Glu
435 440 445

Ile Ile Asp Arg Phe Met Ser Phe Ala Asn Pro Gly His Pro Leu Ser
450 455 460

Val Thr Thr Met Glu Leu Thr Gly Ile Thr Asp Glu Met Val Lys Asp
465 470 475 480

Ala Pro Lys Pro Asp Glu Val Leu Ala Arg Phe Val Asp Trp Ala Gly
485 490 495

Asp Ala Thr Leu Val Ala His Asn Ala Ser Phe Asp Ile Gly Phe Leu
500 505 510

Asn Ala Gly Leu Ala Arg Met Gly Arg Gly Lys Ile Ala Asn Pro Val
515 520 525

Ile Asp Thr Leu Glu Leu Ala Arg Phe Leu Tyr Pro Asp Leu Lys Asn
530 535 540

His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
545 550 555 560

His His Arg Ala Ile Tyr Asp Ala Glu Ala Thr Gly His Leu Leu Met
565 570 575

Arg Leu Leu Lys Glu Ala Glu Glu Arg Gly Ile Leu Phe His Asp Glu
580 585 590

Leu Asn Ser Arg Thr His Ser Glu Ala Ser Tyr Arg Leu Ala Arg Pro
595 600 605

Phe His Val Thr Leu Leu Ala Gln Asn Glu Thr Gly Leu Lys Asn Leu
610 615 620

Phe Lys Leu Val Ser Leu Ser His Ile Gln Tyr Phe His Arg Val Pro
625 630 635 640

Arg Ile Pro Arg Ser Val Leu Val Lys His Arg Asp Gly Leu Leu Val
645 650 655

Gly Ser Gly Cys Asp Lys Gly Glu Leu Phe Asp Asn Leu Ile Gln Lys
660 665 670

Ala Pro Glu Glu Val Glu Asp Ile Ala Arg Phe Tyr Asp Phe Leu Glu
675 680 685

Val His Pro Pro Asp Val Tyr Lys Pro Leu Ile Glu Met Asp Tyr Val
690 695 700

Lys Asp Glu Glu Met Ile Lys Asn Ile Ile Arg Ser Ile Val Ala Leu
705 710 715 720

Gly Glu Lys Leu Asp Ile Pro Val Val Ala Thr Gly Asn Val His Tyr
725 730 735

Leu Asn Pro Glu Asp Lys Ile Tyr Arg Lys Ile Leu Ile His Ser Gln
740 745 750

Gly Gly Ala Asn Pro Leu Asn Arg His Glu Leu Pro Asp Val Tyr Phe
755 760 765

Arg Thr Thr Asn Glu Met Leu Asp Cys Phe Ser Phe Leu Gly Pro Glu
770 775 780

Lys Ala Lys Glu Ile Val Val Asp Asn Thr Gln Lys Ile Ala Ser Leu
785 790 795 800

Ile Gly Asp Val Lys Pro Ile Lys Asp Glu Leu Tyr Thr Pro Arg Ile
805 810 815

Glu Gly Ala Asp Glu Glu Ile Arg Glu Met Ser Tyr Arg Arg Ala Lys
820 825 830

Glu Ile Tyr Gly Asp Pro Leu Pro Lys Leu Val Glu Glu Arg Leu Glu
835 840 845

Lys Glu Leu Lys Ser Ile Ile Gly His Gly Phe Ala Val Ile Tyr Leu
850 855 860

Ile Ser His Lys Leu Val Lys Lys Ser Leu Asp Asp Gly Tyr Leu Val
865 870 875 880

Gly Ser Arg Gly Ser Val Gly Ser Ser Phe Val Ala Thr Met Thr Glu
885 890 895

Ile Thr Glu Val Asn Pro Leu Pro Pro His Tyr Val Cys Pro Asn Cys
900 905 910

Lys His Ser Glu Phe Phe Asn Asp Gly Ser Val Gly Ser Gly Phe Asp
915 920 925

Leu Pro Asp Lys Asn Cys Pro Arg Cys Gly Thr Lys Tyr Lys Lys Asp
930 935 940

Gly His Asp Ile Pro Phe Glu Thr Phe Leu Gly Phe Lys Gly Asp Lys
945 950 955 960

Val Pro Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Pro Arg Ala
965 970 975

His Asn Tyr Thr Lys Val Leu Phe Gly Glu Asp Asn Val Tyr Arg Ala
980 985 990

Gly Thr Ile Gly Thr Val Ala Asp Lys Thr Ala Tyr Gly Phe Val Lys
995 1000 1005

Ala Tyr Ala Ser Asp His Asn Leu Glu Leu Arg Gly Ala Glu Ile Asp
1010 1015 1020

Leu Ala Ala Gly Cys Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro
1025 1030 1035 1040

Gly Gly Ile Ile Val Val Pro Asp Tyr Met Glu Ile Tyr Asp Phe Thr
1045 1050 1055

Pro Ile Gln Tyr Pro Ala Asp Asp Thr Ser Ser Glu Trp Arg Thr Thr
1060 1065 1070

His Phe Asp Phe His Ser Ile His Asp Asn Leu Leu Lys Leu Asp Ile
1075 1080 1085

Leu Gly His Asp Asp Pro Thr Val Ile Arg Met Leu Gln Asp Leu Ser
1090 1095 1100

Gly Ile Asp Pro Lys Thr Ile Pro Thr Asp Asp Pro Asp Val Met Gly
1105 1110 1115 1120

Ile Phe Ser Ser Thr Glu Pro Leu Gly Val Thr Pro Glu Gln Ile Met
1125 1130 1135

Cys Asn Val Gly Thr Ile Gly Ile Pro Glu Phe Gly Thr Arg Phe Val
1140 1145 1150

Arg Gln Met Leu Glu Glu Thr Arg Pro Lys Thr Phe Ser Glu Leu Val
1155 1160 1165

Gln Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Gly Asn Ala
1170 1175 1180

Gln Glu Leu Ile Gln Asn Gly Thr Cys Thr Leu Ser Glu Val Ile Gly
1185 1190 1195 1200

Cys Arg Asp Asp Ile Met Val Tyr Leu Ile Tyr Arg Gly Leu Glu Pro
1205 1210 1215

Ser Leu Ala Phe Lys Ile Met Glu Ser Val Arg Lys Gly Lys Leu
1220 1225 1230

Thr Pro Glu Phe Glu Ala Glu Met Arg Lys His Asp Val Pro Glu Trp
1235 1240 1245

Tyr Ile Asp Ser Cys Lys Ile Lys Tyr Met Phe Pro Lys Ala His
1250 1255 1260

Ala Ala Ala Tyr Val Leu Met Ala Val Arg Ile Ala Tyr Phe Lys Val
1265 1270 1275 1280

His His Pro Leu Leu Tyr Tyr Ala Ser Tyr Phe Thr Val Arg Ala Glu
1285 1290 1295

Asp Phe Asp Leu Asp Ala Met Ile Lys Gly Ser Pro Ala Ile Arg Lys
1300 1305 1310

Arg Ile Glu Glu Ile Asn Ala Lys Gly Ile Gln Ala Thr Ala Lys Glu
1315 1320 1325

Lys Ser Leu Leu Thr Val Leu Glu Val Ala Leu Glu Met Cys Glu Arg
1330 1335 1340

Gly Phe Ser Phe Lys Asn Ile Asp Leu Tyr Arg Ser Gln Ala Thr Glu
1345 1350 1355 1360

Phe Val Ile Asp Gly Asn Ser Leu Ile Pro Pro Phe Asn Ala Ile Pro
1365 1370 1375

Gly Leu Gly Thr Asn Val Ala Gln Ala Ile Val Arg Ala Arg Glu Glu
1380 1385 1390

Gly Glu Phe Leu Ser Lys Glu Asp Leu Gln Gln Arg Gly Lys Leu Ser
 1395 1400 1405

 Lys Thr Leu Leu Glu Tyr Leu Glu Ser Arg Gly Cys Leu Asp Ser Leu
 1410 1415 1420

 Pro Asp His Asn Gln Leu Ser Leu Phe
 1425 1430

 <210> 185
 <211> 199
 <212> PRT
 <213> *Thermus thermophilus*

 <400> 185
 Thr Pro Lys Gly Lys Asp Leu Val Arg His Leu Glu Asn Arg Ala Lys
 1 5 10 15

 Arg Leu Gly Leu Arg Leu Pro Gly Gly Val Ala Gln Tyr Leu Ala Ser
 20 25 30

 Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala
 35 40 45

 Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala
 50 55 60

 Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu
 65 70 75 80

 Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu Gly Arg Leu Lys Glu Glu
 85 90 95

 Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala
 100 105 110

 Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg Glu Met Pro Arg Pro Lys
 115 120 125

 Glu Glu Asp Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys
 130 135 140

 Ala Leu Leu Glu Ala Ala Arg Arg Leu Thr Glu Glu Ala Leu Lys Glu
 145 150 155 160

 Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg Ala Lys Gly Lys

165

170

175

Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu Arg Leu Ala Arg Pro
180 185 190

Ala Gly Gln Pro Arg Val Asp
195

<210> 186

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 186

27

gccccagttacc tcgcctccct cgaggggg

<210> 187

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 187

27

ggccccccttg gccttctcggt cctccat

<210> 188

<211> 331

<212> DNA

<213> Thermus thermophilus

<400> 188

agactcgagg ccctggaggcg ggagctggag aagcttgccc tcctctcccc acccctcacc 60
ctggagaagg tggagaagggt ggtggccctg aggccccccc tcacgggctt tgacctggtg 120
cgctccgtcc tggagaagga ccccaaggag gccctctgc gcctcaggcg cctcaggag 180
gagggggagg agcccctcag gtcctcggg gccctctcct ggcagttcgc ctcctcgcc 240
cgggccttct tcctctccg gaaaaacccc aggcccaagg aggaggacct cgcccgctc 300
gaggcccacc cctacgccgc caagaaggcc a 331

<210> 189

160

<211> 110
<212> PRT
<213> *Thermus thermophilus*

<400> 189
Arg Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala Leu Leu Ser
1 5 10 15
Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala Leu Arg Pro
20 25 30
Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu Lys Asp Pro
35 40 45
Lys Glu Ala Leu Leu Arg Leu Arg Arg Leu Arg Glu Glu Gly Glu Glu
50 55 60
Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala Leu Leu Ala
65 70 75 80
Arg Ala Phe Phe Leu Leu Arg Glu Asn Pro Arg Pro Lys Glu Glu Asp
85 90 95
Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys Ala
100 105 110

<210> 190
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 190
gtggtgtcta gacatcataa cggttctggc a 31

<210> 191
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 191

gagggccacc actttctcca ctttctc

27

<210> 192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 192
ctccgtcctg gagaaggacc ccaag

25

<210> 193
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<221> primer_bind
<222> (15)
<223> S at position 15 can be either C or G

<220>
<221> primer_bind
<222> (27)
<223> S at position 27 can be either C or G

<400> 193
cgcgaattca acgcsctcct caagacsct

29

<210> 194
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 194
gacacttaac atatggtcat cgcccttaccc g

31

<210> 195
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 195
gtgtgtgaat tcgggtcaac gggcgaggcg gaggaccg

38

<210> 196
<211> 10
<212> PRT
<213> Deinococcus radiodurans

<400> 196
Val Ile Leu Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 197
<211> 10
<212> PRT
<213> Methanococcus jannaschii

<400> 197
Tyr Leu Ile Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 198
<211> 10
<212> PRT
<213> Thermotoga maritima

<400> 198
Leu Val Leu Asn Pro Gly Ser Ala Gly Arg
1 5 10

<210> 199
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 199
ctggtaacc cgggctccgt gggccagc

28

<210> 200
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 200
Leu Leu Val Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 201
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 201
ctcgaggagc ttgaggaggg tggc 27

<210> 202
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 202
Ala Asn Thr Leu Leu Lys Leu Leu Glu
1 5

<210> 203
<211> 32
<212> PRT

<213> *Deinococcus radiodurans*

<400> 203

Gly	Phe	Gly	Gly	Val	Gln	Leu	His	Ala	Ala	His	Gly	Tyr	Leu	Leu	Ser
1				5											15
Gln Phe Leu Ser Pro Arg His Asn Val Arg Glu Asp Glu Tyr Gly Gly															
~ 20 25 30															

<210> 204

<211> 32

<212> PRT

<213> *Caenorhabditis elegans*

<400> 204

Gly	Phe	Asp	Gly	Ile	Gln	Leu	His	Gly	Ala	His	Gly	Tyr	Leu	Leu	Ser
1				5											15
Gln Phe Thr Ser Pro Thr Thr Asn Lys Arg Val Asp Lys Tyr Gly Gly															
~ 20 25 30															

<210> 205

<211> 32

<212> PRT

<213> *Pseudomonas aeruginosa*

<400> 205

Gly	Phe	Ser	Gly	Val	Glu	Ile	His	Ala	Ala	His	Gly	Tyr	Leu	Leu	Ser
1				5											15
Gln Phe Leu Ser Pro Leu Ser Asn Arg Arg Ser Asp Ala Trp Gly Gly															
~ 20 25 30															

<210> 206

<211> 32

<212> PRT

<213> Archaeoglobus fulgidus

<400> 206
Gly Phe Asp Ala Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15
Glu Phe Ile Ser Pro His Val Asn Arg Arg Lys Asp Glu Tyr Gly Gly
20 25 30

<210> 207

<211> 30

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

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catcctggac tcggccacc tcctcaccga 30

<210> 208

<211> 9

<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 208
Ile Leu Asp Ser Ala His Leu Leu Thr
1 5

<210> 209

<211> 33

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 209
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33

<210> 210
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 210
Val Glu Leu His Ala Ala His Gly Tyr Leu Leu
1 5 10

<210> 211
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<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<400> 211
ggctttccca tatggctcta cacccggctc ac

32

<210> 212
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<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<400> 212
gcgtggatcc acggtcatgt ctctaagtc

29